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OM protein - protein search, using sw model

Run on: July 13, 2005, 07:46:47 ; Search time 43 Seconds (without alignments)

539.904 Million cell updates/sec

Title: US-09-263-689-4

Perfect score: 311

Sequence: 1 MAFSGSQAPYLSPAVPFSGT.....LPTINRLEVGGDIQIQLTHVQT 311

Scoring table: OLIGO

Gapext 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/8CTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match | Length | DB ID | Description |
|------------|-------|-------|-------|--------|-------------------|-----------------------|
| 1 | 311 | 100.0 | 311 | 3 | US-09-946-914-4 | Sequence 4, Appli |
| 2 | 311 | 100.0 | 311 | 4 | US-09-656-450-4 | Sequence 4, Appli |
| 3 | | | 355 | 4 | US-09-326-402C-18 | Sequence 18, Appli |
| 4 | 163 | 52.4 | 378 | 4 | US-09-854-133-439 | Sequence 439, Appli |
| 5 | 148 | 47.6 | 168 | 4 | US-09-401-064-199 | Sequence 199, Appli |
| 6 | 148 | 47.6 | 301 | 4 | US-09-559-023-4 | Sequence 4, Appli |
| 7 | 87 | 28.0 | 323 | 4 | US-09-326-402C-19 | Sequence 19, Appli |
| 8 | 69 | 22.2 | 145 | 2 | US-08-788-584-1 | Sequence 1, Appli |
| 9 | 69 | 22.2 | 149 | 2 | US-08-788-584-3 | Sequence 3, Appli |
| 10 | 22 | 7.1 | 322 | 4 | US-09-559-023-2 | Sequence 2, Appli |
| 11 | 20 | 6.4 | 145 | 2 | US-08-788-584-5 | Sequence 5, Appli |
| 12 | 20 | 6.4 | 145 | 3 | US-08-946-914-12 | Sequence 12, Appli |
| 13 | 20 | 6.4 | 145 | 4 | US-09-656-450-12 | Sequence 12, Appli |
| 14 | 20 | 6.4 | 145 | 4 | US-09-557-170A-3 | Sequence 3, Appli |
| 15 | 12 | 3.9 | 262 | 3 | US-08-946-914-14 | Sequence 14, Appli |
| 16 | 12 | 3.9 | 262 | 4 | US-09-656-450-14 | Sequence 14, Appli |
| 17 | 10 | 3.2 | 275 | 4 | US-09-557-170A-25 | Sequence 25, Appli |
| 18 | 10 | 3.2 | 296 | 4 | US-09-557-170A-27 | Sequence 27, Appli |
| 19 | 10 | 3.2 | 324 | 3 | US-08-946-914-11 | Sequence 11, Appli |
| 20 | 10 | 3.2 | 324 | 4 | US-09-656-450-11 | Sequence 11, Appli |
| 21 | 10 | 3.2 | 336 | 3 | US-09-131-648-1 | Sequence 1, Appli |
| 22 | 9 | 2.9 | 422 | 4 | US-09-0767-425-72 | Sequence 42572, Appli |
| 23 | 8 | 2.6 | 43 | 4 | US-08-875-553D-43 | Sequence 43, Appli |
| 24 | 8 | 2.6 | 45 | 4 | US-08-175-553D-41 | Sequence 41, Appli |
| 25 | 8 | 2.6 | 45 | 4 | US-08-875-553D-42 | Sequence 42, Appli |
| 26 | 8 | 2.6 | 46 | 4 | US-08-875-553D-40 | Sequence 40, Appli |
| | 8 | 2.6 | 143 | 4 | US-09-877-790-1 | Sequence 1, Appli |

ALIGNMENTS

RESULT 1
US-09-946-914-4
Sequence 4, Application US/08946914
; Patent No. 6027936

GENERAL INFORMATION:

APPLICANT: Ni, Jian
APPLICANT: Gentt, Reiner L.
APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: Galletion 8, 9, 10 and 10SV

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein, & Fox P.L.L.C.
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/946,914
FILING DATE: Herewith
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/028,093
FILING DATE: 09-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Steffe, Eric K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488-0560001/EKS/SGW

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-312-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 311 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-946-914-4

Qy

Query 1 MAFSGSQAPYLSPAVPFSGTPIQGLQDGLOITNGTVLSSSGTRAVNPOTGFSNDIAF 60

1 MAFSGSQAPYLSPAVPFGSTIQQGLQDGQITVNGTIVLSSGTRFAVNFTQGFSGNDIAF 60
 61 HFNPRFEDGYYVVCNTROQSGWPEERKTHMPFKGMPFDLCPFVQSSPFKVNNGILFV 120
 61 HFNPRFEDGYYVVCNTROQSGWPEERKTHMPFKGMPFDLCPFVQSSPFKVNNGILFV 120

RESULT 3
 US-09-326-402C-18
 ; Sequence 18, Application US/09326402C
 ; GENERAL INFORMATION:
 ; Patent No. 6759192
 ; APPLICANT: Bouquelet, Lydie
 ; APPLICANT: Chumakov, Ilyy
 ; APPLICANT: Blumenfeld, Marta
 ; TITLE OF INVENTION: Polymorphic Markers of Prostate Carcinoma Tumor Antigen-1 (PCTA-1)
 ; FILE REFERENCE: GEN-T112XCL
 ; CURRENT APPLICATION NUMBER: US/09/326,402C
 ; CURRENT FILING DATE: 1999-06-04
 ; PRIORITY APPLICATION NUMBER: 60/088,187
 ; PRIORITY FILING DATE: 1998-06-05
 ; PRIORITY APPLICATION NUMBER: 60/102,324
 ; PRIORITY FILING DATE: 1998-09-28
 ; NUMBER OF SEQ ID NOS: 22
 ; SEQ ID NO 18
 ; LENGTH: 355
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (1) .. (355)
 ; OTHER INFORMATION: amino acid sequence of gal9-1
 US-09-326-402C-18

Qy 121 QYFIRVPFRVDTISVNGSVQLSISFQQTIVHTVQSGQMFSTPAIPMMYPHAP 180
 Db 121 QYFIRVPFRVDTISVNGSVQLSISFQQTIVHTVQSGQMFSTPAIPMMYPHAP 180
 Qy 121 QYFIRVPFRVDTISVNGSVQLSISFQQTIVHTVQSGQMFSTPAIPMMYPHAP 180
 Db 121 QYFIRVPFRVDTISVNGSVQLSISFQQTIVHTVQSGQMFSTPAIPMMYPHAP 180
 Qy 181 MPFITTIGLGLYPSKSILLSGTVPLSAQFHINICSGNIAFHINPRDENAVRNTQD 240
 Db 181 MPFITTIGLGLYPSKSILLSGTVPLSAQFHINICSGNIAFHINPRDENAVRNTQD 240
 Qy 241 NSWGSBERSLPRKMPFVRGOSFSWVILCAHCLKVAVDQHLPFEYHRLNLPTRLEV 300
 Db 241 NSWGSBERSLPRKMPFVRGOSFSWVILCAHCLKVAVDQHLPFEYHRLNLPTRLEV 300
 Qy 301 GGD1QLTHVQT 311
 Db 301 GGD1QLTHVQT 311

RESULT 2
 US-09-656-450-4
 ; Sequence 4, Application US/09656450
 ; Patent No. 6468768
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Gantz, Reiner L.
 ; APPLICANT: Ruben, Steven M.
 ; TITLE OF INVENTION: Galectin 9 and 10SV Polynucleotides
 ; FILE REFERENCE: 1488.0560003
 ; CURRENT APPLICATION NUMBER: US/09/656,450
 ; CURRENT FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: US 09/263,689
 ; PRIOR FILING DATE: 1999-03-05
 ; PRIOR APPLICATION NUMBER: US 08/946,914
 ; PRIOR FILING DATE: 1997-10-09
 ; PRIOR APPLICATION NUMBER: US 60/028,093
 ; PRIOR FILING DATE: 1996-10-09
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 311
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-656-450-4

Query Match 52.4%; Score 163; DB 4; Length 355;
 Best Local Similarity 100.0%; Pred. No. 3..153; Mismatches 0; Indels 0; Gaps 0;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 TQTVIHTVQSGQMFSTPAIPMMYPHAPYPMPPFITTIGLGLYPSKSILLSGTVPTR 208
 Db 193 TQTVIHTVQSGQMFSTPAIPMMYPHAPYPMPPFITTIGLGLYPSKSILLSGTVPTR 252
 Qy 209 RFHINLCSGNHIAFHLPFRDENAVRNTQIDNSWGSBERSLPRKMPFVRGOSFSWVILC 268
 Db 253 RFHINLCSGNHIAFHLPFRDENAVRNTQIDNSWGSBERSLPRKMPFVRGOSFSWVILC 312

Qy 269 EAHC1KVAVDQHLPFEYHRLNLPTRLEVQD1QLTHVQT 311
 Db 313 EAHC1KVAVDQHLPFEYHRLNLPTRLEVQD1QLTHVQT 355

RESULT 4
 US-09-854-133-439
 ; Sequence 439, Application US/09854133
 ; Patent No. 6759108
 ; GENERAL INFORMATION:
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Mohamad, Radouh
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Sechrist, Heather
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 ; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121..475C10
 ; CURRENT APPLICATION NUMBER: US/09/854,133
 ; CURRENT FILING DATE: 2001-05-11
 ; NUMBER OF SEQ ID NOS: 735
 ; SOFTWARE: Fast-SEQ for Windows Version 3.0
 ; SEQ ID NO 439
 ; LENGTH: 378
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-854-133-439

Qy 1 MAFSGSQAPYLSPAVPFGSTIQQGLQDGQITVNGTIVLSSGTRFAVNFTQGFSGNDIAF 60
 Db 1 MAFSGSQAPYLSPAVPFGSTIQQGLQDGQITVNGTIVLSSGTRFAVNFTQGFSGNDIAF 60
 Qy 61 HFNPRFEDGYYVVCNTROQSGWPEERKTHMPFKGMPFDLCPFVQSSPFKVNNGILFV 120
 Db 61 HFNPRFEDGYYVVCNTROQSGWPEERKTHMPFKGMPFDLCPFVQSSPFKVNNGILFV 120
 Qy 121 QYFIRVPFRVDTISVNGSVQLSISFQQTIVHTVQSGQMFSTPAIPMMYPHAP 180
 Db 121 QYFIRVPFRVDTISVNGSVQLSISFQQTIVHTVQSGQMFSTPAIPMMYPHAP 180
 Qy 181 MPFITTIGLGLYPSKSILLSGTVPLSAQFHINICSGNIAFHINPRDENAVRNTQD 240
 Db 181 MPFITTIGLGLYPSKSILLSGTVPLSAQFHINICSGNIAFHINPRDENAVRNTQD 240
 Qy 241 NSWGSBERSLPRKMPFVRGOSFSWVILCAHCLKVAVDQHLPFEYHRLNLPTRLEV 300
 Db 241 NSWGSBERSLPRKMPFVRGOSFSWVILCAHCLKVAVDQHLPFEYHRLNLPTRLEV 300

Query Match 52.4%; Score 163; DB 4; Length 378;
 Best Local Similarity 100.0%; Pred. No. 4.2e-153; Mismatches 0; Indels 0;
 Matches 163; Conservative 0; Mismatches 0; Gaps 0;

Qy 149 TQTVIHTVQSAQPGMESTPAIPPMPPFTTILGLYPSKSILISGTLPQAQ 208
 Ddb 216 TQTVIHTVQSAQPGMESTPAIPPMPPFTTILGLYPSKSILISGTLPQAQ 275

Qy 209 RFHINICSGNIAFHINPRFDENAVRNTQIDNSWGSBRSRSLPRKMPFVRSQFSWILC 268
 Ddb 276 RFHINICSGNIAFHINPRFDENAVRNTQIDNSWGSBRSRSLPRKMPFVRSQFSWILC 335

Qy 269 EAHCLKVAVDQHQLFEXYHRNLNLPTRLEVGDIQLTHYQT 311
 Ddb 336 EAHCLKVAVDQHQLFEXYHRNLNLPTRLEVGDIQLTHYQT 378

RESULT 5
 US-09-401-064-199
 Sequence 199, Application US/09401064
 Patent No. 6623923
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Lodes, Michael J.
 APPLICANT: Sechrist, Heather
 APPLICANT: Benson, Darin R.
 APPLICANT: Magher, Madeline Joy
 APPLICANT: Stolk, John A.
 APPLICANT: Wang, Tonglong
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
 TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
 CURRENT FILING DATE: 1999-09-22
 NUMBER OF SEQ ID NOS: 371
 SEQ ID NO 199
 SOFTWARE: FastSEQ for Windows Version 3.0
 FILE REFERENCE: 210121.471C2
 CURRENT APPLICATION NUMBER: US/09/401,064
 CURRENT FILING DATE: 1999-09-22
 NUMBER OF SEQ ID NOS: 371
 SEQ ID NO 199
 SOFTWARE: FastSEQ for Windows Version 3.0
 LENGTH: 168
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-401-064-199

Query Match 47.6%; Score 148; DB 4; Length 168;
 Best Local Similarity 100.0%; Pred. No. 1.4e-138; Mismatches 0; Indels 0;
 Matches 148; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MAFSGSQAPYLSAPVFSGTIQLGGIQLDGLOIQTNGTIVLSSSGTRFAVNFTQGFSNDIAF 60
 Ddb 7 MAFSGSQAPYLSAPVFSGTIQLGGIQLDGLOIQTNGTIVLSSSGTRFAVNFTQGFSNDIAF 66

Qy 61 HFNPFPEDGGVVCNTROQNGWGPBERKTHMPQKMPFDLCLFLVQSSDFKVMNGILFV 120
 Ddb 67 HFNPFPEDGGVVCNTROQNGWGPBERKTHMPQKMPFDLCLFLVQSSDFKVMNGILFV 126

Qy 121 QYFHRVPFHRVDTISYNGSYVLSYISFQ 148
 Ddb 127 QYFHRVPFHRVDTISYNGSYVLSYISFQ 154

RESULT 6
 US-09-559-023-4
 Sequence 4, Application US/09559023
 Patent No. 6551796
 GENERAL INFORMATION:
 APPLICANT: Abramson, Ruth
 APPLICANT: Leal-Pinto, Edgar
 APPLICANT: Lipowitz, Michael
 TITLE OF INVENTION: NUCLEAR ACID ENCODING URATE TRANSPORTER
 FILE REFERENCE: 070165-0574
 CURRENT APPLICATION NUMBER: US/09/559,023
 CURRENT FILING DATE: 2000-04-27
 PRIOR APPLICATION NUMBER: US/09/221,898

Query Match 28.0%; Score 87; DB 4; Length 323;
 Best Local Similarity 100.0%; Pred. No. 6.6e-76; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFSGSQAPYLSAPVFSGTIQLGGIQLDGLOIQTNGTIVLSSSGTRFAVNFTQGFSNDIAF 60
 Ddb 1 MAFSGSQAPYLSAPVFSGTIQLGGIQLDGLOIQTNGTIVLSSSGTRFAVNFTQGFSNDIAF 60

Qy 61 HFNPFPEDGGVVCNTROQNGWGPBERKTHMPQKMPFDLCLFLVQSSDFKVMNGILFV 87
 Ddb 61 HFNPFPEDGGVVCNTROQNGWGPBERKTHMPQKMPFDLCLFLVQSSDFKVMNGILFV 87

RESULT 7
 US-09-326-402C-19
 Sequence 19, Application US/09326402C
 Patent No. 6755192
 GENERAL INFORMATION:
 APPLICANT: Blumentfeld, Marta
 APPLICANT: Bougueret, Lydie
 APPLICANT: Chumakov, Ilya
 TITLE OF INVENTION: Polymorphic Markers of Prostate Carcinoma Tumor Antigen-1
 FILE REFERENCE: GEN-T112X1
 CURRENT APPLICATION NUMBER: US/09/326,402C
 CURRENT FILING DATE: 1999-06-04
 PRIORITY: 1999-06-04
 PRIORITY NUMBER: 60/088,187
 PRIORITY FILING DATE: 1998-06-05
 PRIORITY NUMBER: 60/102,324
 PRIORITY FILING DATE: 1998-09-28
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 19
 LENGTH: 323
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: MISC_FEATURE
 LOCATION: (1..(323))
 OTHER INFORMATION: amino acid sequence of gal

US-09-326-402C-19

Query Match 28.0%; Score 87; DB 4; Length 323;
 Best Local Similarity 100.0%; Pred. No. 6.6e-76; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFSGSQAPYLSAPVFSGTIQLGGIQLDGLOIQTNGTIVLSSSGTRFAVNFTQGFSNDIAF 60
 Ddb 1 MAFSGSQAPYLSAPVFSGTIQLGGIQLDGLOIQTNGTIVLSSSGTRFAVNFTQGFSNDIAF 60

Sequence 1, Application US/08788584
 Patent No. 5837493
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Goli, Surya K.
 APPLICANT: Bandman, Oiga
 APPLICANT: Hawkins, Phillip R.
 APPLICANT: Petithory, Joanne R.
 TITLE OF INVENTION: NOVEL HUMAN GALECTINS
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/788,584
 FILING DATE: Filed Herewith
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0192 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 145 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-788-584-1

RESULT 9
 Query Match 22.2%; Score 69; DB 2; Length 145;
 Best Local Similarity 100.0%; Pred. No. 2.1e-60;
 Matches 65; Conservative 0; Mismatches 0; Gaps 0;
 Qy 243 WGSEERSLPRKMPFVRGQSSWVILCEAHLKVAVDGQHLEFYHRLNPLTPNRLVEGG 302
 Db 77 WGSEERSLPRKMPFVRGQSSWVILCEAHLKVAVDGQHLEFYHRLNPLTPNRLVEGG 136

Query Match 22.2%; Score 69; DB 2; Length 145;
 Best Local Similarity 100.0%; Pred. No. 2.1e-60;
 Matches 65; Conservative 0; Mismatches 0; Gaps 0;
 Qy 303 DIOQLTHVQT 311
 Db 137 DIOQLTHVQT 145

RESULT 9
 Query Match 7.1%; Score 22; DB 4; Length 322;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 22; Conservative 0; Mismatches 0; Gaps 0;

Qy 46 AVNFGTGFSGNDIAFHNPRLS 67
 Db 45 AVNFGTGFSGNDIAFHNPRLS 66

RESULT 11

US-08-788-584-5

; Sequence 5 , Application US/08788584

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Goli, Surya K.

; APPLICANT: Bandman, Olga

; APPLICANT: Hawkins, Phillip R.

; APPLICANT: Petithory, Joanne R.

; TITLE OF INVENTION: NOVEL HUMAN GALECTINS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSER: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION NUMBER: US/08788584

; APPLICATION NUMBER: US-08/788,584

; FILING DATE: Filed Herewith

; CLASSIFICATION: 436

; PRIOR APPLICATION NUMBER:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PP-0192 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 5 :

; SEQUENCE CHARACTERISTICS:

; LENGTH: 145 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; CLONE: Genbank

; CLONE: 727176

; US-08-788-584-5

; Query Match

; Best Local Similarity 100.0% ; Pred. No. 7e-12 ; Indels 0 ; Gaps 0 ;

; Matches 20 ; Conservative 0 ; Mismatches 0 ;

; CURRENT APPLICATION NUMBER: US-09/656,450

; PRIORITY APPLICATION NUMBER: 1488.0560001

; CURRENT FILING DATE: 2000-09-06

; PRIORITY FILING DATE: 1999-03-05

; PRIORITY APPLICATION NUMBER: US 08/946,914

; PRIORITY FILING DATE: 1997-10-09

; PRIORITY APPLICATION NUMBER: US 60/028,093

; PRIORITY FILING DATE: 1996-10-09

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO: 12

; LENGTH: 145

; TYPE: PRT

; ORGANISM: Rat

; US-09-656-450-12

; TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV Polynucleotides

; RESULT 12

; US-08-946-914-12

; Sequence 12 , Application US/08946914

; Parent No. 6027916

; GENERAL INFORMATION:

; APPLICANT: Gentz, Reiner L.

; APPLICANT: Ruben, Steven M.

; TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV

NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterns, Kessler, Goldstein, & Fox P.L.L.C.
 STREET: 1100 New York Ave., Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC DOS/MS DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/946,914

; FILING DATE: Herewith

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/028,093

; ATTORNEY/AGENT INFORMATION:

; NAME: Steff, Eric K.

; REGISTRATION NUMBER: 36,688

; REFERENCE/DOCKET NUMBER: 1488.0560001/EKS/SGW

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-2500

; TELEFAX: 202-371-2540

; INFORMATION FOR SEQ ID NO: 12 :

; SEQUENCE CHARACTERISTICS:

; LENGTH: 145 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; US-08-946-914-12

; Query Match 6.4% ; Score 20 ; DB 3 ; Length 145 ;

; Best Local Similarity 100.0% ; Pred. No. 7e-12 ; Indels 0 ; Gaps 0 ;

; Matches 20 ; Conservative 0 ; Mismatches 0 ;

; CURRENT APPLICATION NUMBER: US/09/656,450

; PRIORITY APPLICATION NUMBER: 1488.0560001

; CURRENT FILING DATE: 2000-09-06

; PRIORITY FILING DATE: 1999-03-05

; PRIORITY APPLICATION NUMBER: US 08/946,914

; PRIORITY FILING DATE: 1997-10-09

; PRIORITY APPLICATION NUMBER: US 60/028,093

; PRIORITY FILING DATE: 1996-10-09

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO: 12

; LENGTH: 145

; TYPE: PRT

; ORGANISM: Rat

; US-09-656-450-12

; TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV

; RESULT 13

; US-09-656-450-12

; Sequence 12 , Application US/09656450

; Parent No. 6468768

; GENERAL INFORMATION:

; APPLICANT: Ni, Jian

; APPLICANT: Gentz, Reiner L.

; APPLICANT: Ruben, Steven M.

; TITLE OF INVENTION: Galectin 9 and 10SV Polynucleotides

; FILE REFERENCE: 1488.0560003

; CURRENT APPLICATION NUMBER: US/09/656,450

; PRIORITY APPLICATION NUMBER: 1488.0560003

; CURRENT FILING DATE: 2000-09-06

; PRIORITY FILING DATE: 1999-03-05

; PRIORITY APPLICATION NUMBER: US 08/946,914

; PRIORITY FILING DATE: 1997-10-09

; PRIORITY APPLICATION NUMBER: US 60/028,093

; PRIORITY FILING DATE: 1996-10-09

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO: 12

; LENGTH: 145

; TYPE: PRT

; ORGANISM: Rat

; US-09-656-450-12

; TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; APPLICATION NUMBER: US 60/028,093
 FILING DATE: 09-OCT-1996
 ATTORNEY/AGENT/INFORMATION:
 NAME: Steffe, Eric K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488-0560001/EKS/SGW
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 262 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-946-914-14

Query Match 3.9%; Score 12; DB 3; Length 262;
 Best Local Similarity 100.0%; Pred. No. 0.001; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 GNDIAFHENPFRF 66
 ||||| ||||| |||||
 Db 164 GNDIAFHENPFRF 175

Search completed: July 13, 2005, 07:47:39
 Job time : 44 secs

RESULT 14
 US-09-557-170A-3
 Sequence 3, Application US/09557170A
 Patent No. 6605639
 GENERAL INFORMATION:
 APPLICANT: Ni et al.
 TITLE OF INVENTION: Galectin 11
 FILE REFERENCE: PE35aP2
 CURRENT APPLICATION NUMBER: US/09/557,170A
 CURRENT FILING DATE: 2000-04-21
 PRIOR APPLICATION NUMBER: 09/109,864
 PRIOR FILING DATE: 1998-06-06
 PRIOR APPLICATION NUMBER: 09/010,146
 PRIOR FILING DATE: 1998-01-21
 PRIOR APPLICATION NUMBER: 60/034,205
 PRIOR FILING DATE: 1997-01-21
 PRIOR APPLICATION NUMBER: 60/034,204
 PRIOR FILING DATE: 1997-01-21
 PRIOR APPLICATION NUMBER: 60/169,932
 PRIOR FILING DATE: 1999-12-10
 PRIOR APPLICATION NUMBER: 60/130,390
 PRIOR FILING DATE: 1999-04-21
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3
 LENGTH: 145
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-557-170A-3

Query Match 6.4%; Score 20; DB 4; Length 145;
 Best Local Similarity 100.0%; Pred. No. 7e-12; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 220 IAFHLNPRFDENAVVRNTQI 239
 ||||| ||||| ||||| ||||| |||||
 Db 54 IAFHLNPRFDENAVVRNTQI 73

RESULT 15
 US-08-946-914-14
 Sequence 14, Application US/08946914
 Patent No. 6027916
 GENERAL INFORMATION:
 APPLICANT: Ni, Jian
 APPLICANT: Gentz, Reiner L.
 APPLICANT: Ruben, Steven M.
 TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Steerne, Kessler, Goldstein, & Fox P.L.L.C.
 STREET: 1100 New York Ave., Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/946,914
 FILING DATE: Herewith
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:

TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 41
 SEQUENCE CHARACTERISTICS:
 LENGTH: 311 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-263-689-4

Query Match 100.0%; Score 311; DB 9; Length 311;
 Best Local Similarity 100.0%; Pred. No. 1.e-281; Indels 0; Gaps 0;
 Matches 311; Conservative 0; Mismatches 0; SEQ ID NO: 41

Db 1 MAFSGSQAPYLSPAVPFSGTICQGLDGLQITVNGTIVLSSSGTRFAVNFTQGFSGNDIAF 60
 Qy 61 HENPFPEDGGYVNCNTRONGSGPBERKTHMPFQKGMFDLCLCFLVQSSDEKFVNNGILFV 120
 Db 61 HENPFPEDGGYVNCNTRONGSGPBERKTHMPFQKGMFDLCLCFLVQSSDEKFVNNGILFV 120
 Qy 121 QYFHRVPFHRVDTISVNGSVQLSYISFQOTQVHTVQSGQMFSTPAIPPMYPHPAYP 180
 Db 121 QYFHRVPFHRVDTISVNGSVQLSYISFQOTQVHTVQSGQMFSTPAIPPMYPHPAYP 180
 Qy 181 MPFTTILGGLYPSKSILISGTVLPSAQRFHINICSGNHAFLHNPRFDEAVRNTQID 240
 Db 181 MPFTTILGGLYPSKSILISGTVLPSAQRFHINICSGNHAFLHNPRFDEAVRNTQID 240
 Qy 241 NSGSEERSLPRKMPFVRQSFVWILCEAHCLKVAVDQHLPFEYHRLNPTINRLEV 300
 Db 241 NSGSEERSLPRKMPFVRQSFVWILCEAHCLKVAVDQHLPFEYHRLNPTINRLEV 300
 Qy 301 GGDIOQLTHYQT 311
 Db 301 GGDIOQLTHYQT 311

RESULT 3
 US-10-415-586-3
 ; Sequence 3, Application US/10415586
 ; Publication No US2004003346A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YAMASHITA, Mitsuomi
 ; APPLICANT: YAMAMUCHI, Akira
 ; APPLICANT: KAGESHITA, Tohiko
 ; APPLICANT: NAKAMURA, Kananori
 ; APPLICANT: NISHI, No. US20040053346A1
 ; TITLE OF INVENTION: Predicting agent for a metastasis
 ; FILE REFERENCE: 2003-0572A/WNC/0132
 ; CURRENT APPLICATION NUMBER: US/10/415,586
 ; CURRENT FILING DATE: 2003-09-05
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; PRIOR FILING DATE: 2001-10-31
 ; PRIOR APPLICATION NUMBER: JP 2000-335077
 ; PRIOR FILING DATE: 2000-11-01
 ; NUMBER OF SEQ ID NOS: 9
 ; SEQ ID NO 3
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-415-586-3

Query Match 98.4%; Score 306; DB 15; Length 311;
 Best Local Similarity 100.0%; Pred. No. 5.e-279; Mismatches 0; Indels 0; Gaps 0;
 Matches 306; Conservative 0; Software: PatentIn Version 3.0

Qy 6 SQAPYLSPAVPFSGTICQGLDGLQITVNGTIVLSSSGTRFAVNFTQGFSGNDIAFHFNPR 65
 Db 6 SQAPYLSPAVPFSGTICQGLDGLQITVNGTIVLSSSGTRFAVNFTQGFSGNDIAFHFNPR 65
 Qy 66 FEDGGYVNCNTRONGSGPBERKTHMPFQKGMFDLCLCFLVQSSDEKFVNNGILFVQYHR 125
 Db 66 FEDGGYVNCNTRONGSGPBERKTHMPFQKGMFDLCLCFLVQSSDEKFVNNGILFVQYHR 125
 Qy 126 VPFFRVDITISVNGSVQLSYISFQOTQVHTVQSGQMFSTPAIPPMYPHPAYPMPFT 185
 Db 126 VPFFRVDITISVNGSVQLSYISFQOTQVHTVQSGQMFSTPAIPPMYPHPAYPMPFT 185
 Qy 186 TILGGLYPSKSILISGTVLPSAQRFHINICSGNHAFLHNPRFDEAVRNTQIDNSWCS 245
 Db 186 TILGGLYPSKSILISGTVLPSAQRFHINICSGNHAFLHNPRFDEAVRNTQIDNSWCS 245
 Qy 246 EERSLPRKMPFVRQSFVWILCEAHCLKVAVDQHLPFEYHRLNPTINRLEVGGDQ 305
 Db 246 EERSLPRKMPFVRQSFVWILCEAHCLKVAVDQHLPFEYHRLNPTINRLEVGGDQ 305

Query Match 100.0%; Score 311; DB 14; Length 311;
 Best Local Similarity 100.0%; Pred. No. 1.e-281; Indels 0; Gaps 0;
 Matches 311; Conservative 0; Mismatches 0; SEQ ID NO: 60

Qy 1 MAFSGSQAPYLSPAVPFSGTICQGLDGLQITVNGTIVLSSSGTRFAVNFTQGFSGNDIAF 60

RESULT 4

Qy 306 LTHVQT 311
 Db 306 LTHVQT 311

SEQUENCE 2, Application US/09728479
 Patent No. US2002034765A1

GENERAL INFORMATION:
 APPLICANT: KANEKASAKI, SHIRO
 APPLICANT: MATSUMOTO, RYOKI
 APPLICANT: HIRASHIMA, MITSUOMI

TITLE OF INVENTION: EOSINOPHIL CHEMOTACTIC FACTOR
 FILE REFERENCE: 3914-2

CURRENT APPLICATION NUMBER: US/09/728,479
 CURRENT FILING DATE: 2001-08-16
 PRIOR APPLICATION NUMBER: PCT/JP99/02952
 PRIOR APPLICATION NUMBER: JP 10/170698
 PRIOR FILING DATE: 1998-06-02
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 2
 LENGTH: 323
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-728-479-2

Query Match 52.4%; Score 163; DB 9; Length 323;
 Best Local Similarity 100.0%; Pred. No. 1.4e-144;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 TQTVIHTVQSGPQMFSTPAIPPMYPHPAYMPPTTIGLYPSKSILLSGTLPQAQ 208
 Db 161 TQTVIHTVQSGPQMFSTPAIPPMYPHPAYMPPTTIGLYPSKSILLSGTLPQAQ 220

Qy 209 RFHINLCSGNHIAFLNPRDENAVRNTQIDNSGSEERSLPRKMPFVRGQSFVWILC 268
 Db 221 RFHINLCSGNHIAFLNPRDENAVRNTQIDNSGSEERSLPRKMPFVRGQSFVWILC 280

Qy 269 EAHCILKVAVDQQLPEYYHRLNLPTRNLEVGDDIQLTHVQT 311
 Db 281 EAHCILKVAVDQQLPEYYHRLNLPTRNLEVGDDIQLTHVQT 323

RESULT 5

Qy 306 LTHVQT 311
 Db 306 LTHVQT 311

SEQUENCE 141, Application US/10042211A
 Publication No. US2003010719A1

GENERAL INFORMATION:
 APPLICANT: MATSUDA, Akio et al.
 TITLE OF INVENTION: NPKB Activating Gene
 FILE REFERENCE: 1254-0128P
 CURRENT APPLICATION NUMBER: US/10/042,211A
 PRIORITY DATE: 2003-01-11
 PRIOR APPLICATION NUMBER: JP 2000-402288
 PRIOR FILING DATE: 2000-12-28
 PRIOR APPLICATION NUMBER: JP 2001-088912
 PRIOR FILING DATE: 2001-03-26
 PRIOR APPLICATION NUMBER: JP 2001-254018
 PRIOR FILING DATE: 2001-08-24
 PRIOR APPLICATION NUMBER: US 60/258,315
 PRIOR FILING DATE: 2000-12-28
 PRIOR APPLICATION NUMBER: US 60/278,640
 PRIOR FILING DATE: 2001-03-26
 PRIOR APPLICATION NUMBER: US 60/314,385
 NUMBER OF SEQ ID NOS: 182
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 141
 LENGTH: 323
 TYPE: PRT
 ORGANISM: Homo sapiens

US-10-042-211A-141

Query Match 52.4%; Score 163; DB 14; Length 323;
 Best Local Similarity 100.0%; Pred. No. 1.4e-144;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 TQTVIHTVQSGPQMFSTPAIPPMYPHPAYMPPTTIGLYPSKSILLSGTLPQAQ 208
 Db 161 TQTVIHTVQSGPQMFSTPAIPPMYPHPAYMPPTTIGLYPSKSILLSGTLPQAQ 220

Qy 209 RFHINLCSGNHIAFLNPRDENAVRNTQIDNSGSEERSLPRKMPFVRGQSFVWILC 268
 Db 221 RFHINLCSGNHIAFLNPRDENAVRNTQIDNSGSEERSLPRKMPFVRGQSFVWILC 280

Qy 269 EAHCILKVAVDQQLPEYYHRLNLPTRNLEVGDDIQLTHVQT 311
 Db 281 EAHCILKVAVDQQLPEYYHRLNLPTRNLEVGDDIQLTHVQT 323

RESULT 7
 US-10-415-586-2

Sequence 2, Application US/10415586
 GENERAL INFORMATION: US2004005346A1
 APPLICANT: HIRASHIMA, Mitsuomi
 APPLICANT: YANUCHI, Akira
 APPLICANT: KAGESHITA, Toshiro
 APPLICANT: NAKAMURA, Takanori
 APPLICANT: NISHI, No. US0040053346A1
 TITLE OF INVENTION: Predicting agent for a metastasis
 FILE REFERENCE: 2003-0572A/WMC/01322
 CURRENT APPLICATION NUMBER: US10/415,586
 CURRENT FILING DATE: 2003-09-05
 PRIOR APPLICATION NUMBER: PCT/JP01/09561.
 PRIOR FILING DATE: 2001-10-31
 PRIOR APPLICATION NUMBER: JP 2000-335077
 PRIORITY NUMBER: 2000-11-01
 SEQ ID NO: 2
 SOFTWARE: PatentIn Ver. 2.0
 LENGTH: 323
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-415-586-2

Query Match 52.4%; Score 163; DB 15; Length 323;
 Best Local Similarity 100.0%; Pred. No. 1.4e-14; Mismatches 0; Indels 0; Gaps 0;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 TQTVIHTVQASPGMFSTAIPPMYPHAYPMPFITTIGLYPSKSILLSGTVLPSAQ 208
 Db 161 RFHINLCSGNHIAFLHNPREFDENAVRNTQIDNSWGSERSLPRKMPFVRGOSFSWILC 220
 Qy 209 RFHINLCSGNHIAFLHNPREFDENAVRNTQIDNSWGSERSLPRKMPFVRGOSFSWILC 268
 Db 221 RFHINLCSGNHIAFLHNPREFDENAVRNTQIDNSWGSERSLPRKMPFVRGOSFSWILC 280

Qy 269 EAHCLKVAVDGQHLYFEYTHRLNPLTINRLEVGGDIOLTHVQT 311
 Db 281 EAHCLKVAVDGQHLYFEYTHRLNPLTINRLEVGGDIOLTHVQT 323

RESULT 9
 US-10-024-298A-141
 Sequence 141, Application US/10024298A
 Publication No. US20040214167A9
 GENERAL INFORMATION:
 APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
 APPLICANT: AKIO MATSUDA
 APPLICANT: Goichi HONDA
 APPLICANT: Shuji MURAMATSU
 APPLICANT: Yukiko NAGANO
 TITLE OF INVENTION: NF-K B Activating Gene
 FILE REFERENCE: 1254-0191P
 CURRENT APPLICATION NUMBER: US/10/024,298A
 CURRENT FILING DATE: 2003-04-08
 PRIOR APPLICATION NUMBER: 60/314,385
 PRIOR FILING DATE: 2001-08-24
 PRIOR APPLICATION NUMBER: 60/278,641
 PRIOR FILING DATE: 2001-03-26
 PRIOR APPLICATION NUMBER: 60/258,315
 PRIOR FILING DATE: 2000-12-28
 PRIOR APPLICATION NUMBER: JP54018/2001
 PRIOR FILING DATE: 2001-08-24
 PRIOR APPLICATION NUMBER: JP0088912/2001
 PRIOR FILING DATE: 2001-03-26
 PRIOR APPLICATION NUMBER: JP022288/2000
 PRIOR FILING DATE: 2000-12-28
 NUMBER OF SEQ ID: NOS: 182
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 141
 LENGTH: 323
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-024-298A-141

Query Match 52.4%; Score 163; DB 16; Length 323;
 Best Local Similarity 100.0%; Pred. No. 1.4e-14;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 TQTVIHTVQASPGMFSTAIPPMYPHAYPMPFITTIGLYPSKSILLSGTVLPSAQ 208
 Db 161 RFHINLCSGNHIAFLHNPREFDENAVRNTQIDNSWGSERSLPRKMPFVRGOSFSWILC 220
 Qy 209 RFHINLCSGNHIAFLHNPREFDENAVRNTQIDNSWGSERSLPRKMPFVRGOSFSWILC 268
 Db 221 RFHINLCSGNHIAFLHNPREFDENAVRNTQIDNSWGSERSLPRKMPFVRGOSFSWILC 280

Qy 269 EAHCLKVAVDGQHLYFEYTHRLNPLTINRLEVGGDIOLTHVQT 311
 Db 281 EAHCLKVAVDGQHLYFEYTHRLNPLTINRLEVGGDIOLTHVQT 323

RESULT 10
 US-10-376-133-18
 Sequence 18, Application US/10376133
 Publication No. US2003016565A1
 GENERAL INFORMATION:
 APPLICANT: EXELLIXIS, INC.
 TITLE OF INVENTION: LGALS AS MODIFIERS OF THE CHK PATHWAY AND METHODS OF USE
 Query Match 52.4%; Score 163; DB 15; Length 323;
 Best Local Similarity 100.0%; Pred. No. 1.4e-14;

FILE REFERENCE: EX03-014C
 CURRENT APPLICATION NUMBER: US/10/376,133
 CURRENT FILING DATE: 2003-02-28
 PRIORITY NUMBER: US 60/360,757
 PRIORITY FILING DATE: 2002-03-01
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: Patent in version 3.2
 SEQ ID NO 18
 LENGTH: 355
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-376-133-18

Query Match 52.4%; Score 163; DB 14; Length 355;
 Best Local Similarity 100.0%; Pred. No. 1.6e-144; Indels 0; Gaps 0;
 Matches 163; Conservative 0; Mismatches 0; Indel s 0; Gaps 0;

Qy 149 TQTVIHTVQSAQGMESTPAIPPMYPHAYPMPFITTIGLYPSKSILLSGTVLPSAQ 208
 Db 193 TQTVIHTVQSAQGMESTPAIPPMYPHAYPMPFITTIGLYPSKSILLSGTVLPSAQ 252

Qy 209 RFHINLCSGNHIAFHINPFDENAVRTNTQDMSWSEERSLPRKMPFVRCQFSVWILC 268
 Db 253 RFHINLCSGNHIAFHINPFDENAVRTNTQDMSWSEERSLPRKMPFVRCQFSVWILC 312

Qy 269 EAHCLKVAVDGQHLFEYTHRLNLPTINRLEVGDIQLTHYQT 311
 Db 313 EAHCLKVAVDGQHLFEYTHRLNLPTINRLEVGDIQLTHYQT 355

Query Match 52.4%; Score 163; DB 15; Length 355;
 Best Local Similarity 100.0%; Pred. No. 1.6e-144; Indels 0; Gaps 0;
 Matches 163; Conservative 0; Mismatches 0; Indel s 0; Gaps 0;

Qy 149 TQTVIHTVQSAQGMESTPAIPPMYPHAYPMPFITTIGLYPSKSILLSGTVLPSAQ 208
 Db 193 TQTVIHTVQSAQGMESTPAIPPMYPHAYPMPFITTIGLYPSKSILLSGTVLPSAQ 252

Qy 209 RFHINLCSGNHIAFHINPFDENAVRTNTQDMSWSEERSLPRKMPFVRCQFSVWILC 268
 Db 253 RFHINLCSGNHIAFHINPFDENAVRTNTQDMSWSEERSLPRKMPFVRCQFSVWILC 312

Qy 269 EAHCLKVAVDGQHLFEYTHRLNLPTINRLEVGDIQLTHYQT 311
 Db 313 EAHCLKVAVDGQHLFEYTHRLNLPTINRLEVGDIQLTHYQT 355

RESULT 1.3
 US-10-415-586-1
 Sequence 1, Application US/10415586
 Publication No. US20040053346A1
 GENERAL INFORMATION:
 APPLICANT: HIRASHIMA, Mitsuomi
 APPLICANT: YAMAUCHI, Akira
 APPLICANT: KAGESHITA, Toshiro
 APPLICANT: NAKAMURA, Takanori
 APPLICANT: NISHI, No. US20040053346A1
 TITLE OF INVENTION: Predicting agent for a metastasis
 FILE REFERENCE: 2003-0572A/PMC/03332
 CURRENT APPLICATION NUMBER: US/10/415,586
 CURRENT FILING DATE: 2003-09-05
 PRIORITY NUMBER: PCT/JP01/09561
 PRIORITY FILING DATE: 2001-10-31
 PRIORITY NUMBER: JP 2000-3350577
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: Patent in version 2.0
 SEQ ID NO 1
 LENGTH: 355
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-415-586-1

Query Match 52.4%; Score 163; DB 15; Length 355;
 Best Local Similarity 100.0%; Pred. No. 1.6e-144; Indels 0; Gaps 0;
 Matches 163; Conservative 0; Mismatches 0; Indel s 0; Gaps 0;

Qy 149 TQTVIHTVQSAQGMESTPAIPPMYPHAYPMPFITTIGLYPSKSILLSGTVLPSAQ 208
 Db 193 TQTVIHTVQSAQGMESTPAIPPMYPHAYPMPFITTIGLYPSKSILLSGTVLPSAQ 252

Qy 209 RFHINLCSGNHIAFHINPFDENAVRTNTQDMSWSEERSLPRKMPFVRCQFSVWILC 268
 Db 253 RFHINLCSGNHIAFHINPFDENAVRTNTQDMSWSEERSLPRKMPFVRCQFSVWILC 312

Qy 269 EAHCLKVAVDGQHLFEYTHRLNLPTINRLEVGDIQLTHYQT 311
 Db 313 EAHCLKVAVDGQHLFEYTHRLNLPTINRLEVGDIQLTHYQT 355

RESULT 1.3
 US-10-633-035-6
 Sequence 6, Application US/10633035
 Publication No. US20040068104A1
 GENERAL INFORMATION:
 APPLICANT: Seisi Kato
 APPLICANT: Yamaguchi Kimura
 APPLICANT: Shingo Sekine
 APPLICANT: Kouju Kamata
 TITLE OF INVENTION: PROTEINS
 FILE REFERENCE: GIN-6707CPUS
 CURRENT APPLICATION NUMBER: US/10/633,035
 CURRENT FILING DATE: 2003-08-04
 PRIORITY NUMBER: US/09/485,951
 PRIORITY NUMBER: 9-226468
 PRIORITY NUMBER: 1997-08-22
 PRIORITY NUMBER: 1998-08-19
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: Patent in version 2.0
 SEQ ID NO 6
 LENGTH: 355
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-633-035-6

Query Match 52.4%; Score 163; DB 15; Length 355;
 Best Local Similarity 100.0%; Pred. No. 1.6e-14;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 APPLICANT: Mohamath, Radoh
 APPLICANT: Algate, Paul A.
 APPLICANT: Scristi, Heather
 APPLICANT: Indriis, Carol Joseph
 APPLICANT: Benson, Darin R.
 APPLICANT: Elliot, Mark
 APPLICANT: Mannion, Jane
 APPLICANT: Kalos, Michael D.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
 CURRENT APPLICATION NUMBER: US/09/738-973
 CURRENT FILING DATE: 2000-12-14
 NUMBER OF SEQ ID NOS: 587
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 439
 LENGTH: 378
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-738-973-439

Query Match 52.4%; Score 163; DB 9; Length 378;
 Best Local Similarity 100.0%; Pred. No. 1.6e-14;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 APPLICANT: Blumenfeld, Marta
 APPLICANT: Bouquelaret, Lydie
 APPLICANT: Chumakov, Ily
 TITLE OF INVENTION: Polymorphic Markers of Prostate Carcinoma Tumor Antigen-1 (PCTA-1)
 FILE REFERENCE: GEN_T112XCL
 CURRENT APPLICATION NUMBER: US/10/856,888
 CURRENT FILING DATE: 2004-05-27
 PRIORITY APPLICATION NUMBER: US/09/326,402
 PRIORITY FILING DATE: 1999-06-04
 PRIORITY FILING DATE: 1998-06-05
 PRIORITY FILING DATE: 1998-09-28
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 18
 LENGTH: 355
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: MISC_FEATURE
 LOCATION: (1)..(355)
 OTHER INFORMATION: amino acid sequence of gal9-1
 US-10-856-888-18

Query Match 52.4%; Score 163; DB 16; Length 355;
 Best Local Similarity 100.0%; Pred. No. 1.6e-14;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 APPLICANT: Reed, Steven G.
 APPLICANT: Henderson, Robert A.
 APPLICANT: Lodes, Michael J.
 APPLICANT: Fling, Steven P.

RESULT 15
 US-09-738-973-439
 Sequence 439, Application US/09738973
 Patent No. US200101563A1
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Henderson, Robert A.
 APPLICANT: Lodes, Michael J.
 APPLICANT: Fling, Steven P.

Query Match 52.4%; Score 163; DB 15; Length 355;
 Best Local Similarity 100.0%; Pred. No. 1.6e-14;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 APPLICANT: Mohamath, Radoh
 APPLICANT: Algate, Paul A.
 APPLICANT: Scristi, Heather
 APPLICANT: Indriis, Carol Joseph
 APPLICANT: Benson, Darin R.
 APPLICANT: Elliot, Mark
 APPLICANT: Mannion, Jane
 APPLICANT: Kalos, Michael D.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
 CURRENT APPLICATION NUMBER: US/09/738-973
 CURRENT FILING DATE: 2000-12-14
 NUMBER OF SEQ ID NOS: 587
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 439
 LENGTH: 378
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-738-973-439

Query Match 52.4%; Score 163; DB 9; Length 378;
 Best Local Similarity 100.0%; Pred. No. 1.6e-14;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 APPLICANT: Blumenfeld, Marta
 APPLICANT: Bouquelaret, Lydie
 APPLICANT: Chumakov, Ily
 TITLE OF INVENTION: Polymorphic Markers of Prostate Carcinoma Tumor Antigen-1 (PCTA-1)
 FILE REFERENCE: GEN_T112XCL
 CURRENT APPLICATION NUMBER: US/10/856,888
 CURRENT FILING DATE: 2004-05-27
 PRIORITY APPLICATION NUMBER: US/09/326,402
 PRIORITY FILING DATE: 1999-06-04
 PRIORITY FILING DATE: 1998-06-05
 PRIORITY FILING DATE: 1998-09-28
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 18
 LENGTH: 355
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: MISC_FEATURE
 LOCATION: (1)..(355)
 OTHER INFORMATION: amino acid sequence of gal9-1
 US-10-856-888-18

Query Match 52.4%; Score 163; DB 16; Length 355;
 Best Local Similarity 100.0%; Pred. No. 1.6e-14;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 APPLICANT: Reed, Steven G.
 APPLICANT: Henderson, Robert A.
 APPLICANT: Lodes, Michael J.
 APPLICANT: Fling, Steven P.

RESULT 15
 US-09-738-973-439
 Sequence 439, Application US/09738973
 Patent No. US200101563A1
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Henderson, Robert A.
 APPLICANT: Lodes, Michael J.
 APPLICANT: Fling, Steven P.

| Copyright (c) 1993 - 2005 Compugen Ltd. | GenCore version 5.1.6 | Q6dgj1 | brachydanio | | |
|--|--|-------------|--------------|-------|--------------------------|
| OM protein - protein search, using sw model | | Q7t120 | brachydanio | | |
| Run on: | July 13, 2005, 07:46:47 ; Search time 174 Seconds (without alignments) | P47845 | oryctolagus | | |
| Title: | US-09-263-689-4 | P17931 | homo sapien | | |
| Perfect score: | 311 | Q6fgj0 | homo sapien | | |
| Sequence: | 1 MAEFSQAPYLSPAVPFGST. LPTINRLLEVGGDIQLTHVQT 311 | Q6ib7 | homo sapien | | |
| Scoring table: | OLIGO | Q6nvh9 | homo sapien | | |
| GapOp | 60.0 , Gapext 60.0 | P16110 | mus musculu | | |
| Searched: | 1612378 seqs, 512079187 residues | Q8c253 | mus musculu | | |
| Word size : | 0 | Q8d486 | canis famili | | |
| Total number of hits satisfying chosen parameters: | 1612378 | Q8gq87 | canis famili | | |
| Minimum DB seq length: 0 | | Q86g87 | homo sapien | | |
| Maximum DB seq length: 2000000000 | | Q86b77 | mus musculu | | |
| Post-processing: Listing first 45 summaries | | Q8pbv2 | brachydanio | | |
| Database : | UniProt_03:* | Q7t118 | brachydanio | | |
| | 1: uniprot_sprot:* | | | | |
| | 2: uniprot_trembl:* | | | | |
| Pred. | No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | | | | |
| SUMMARIES | | | | | |
| Result No. | Score | Query Match | Length | DB ID | Description |
| 1 | 311 | 100.0 | 311 | 2 | Q8wyQ7 homo sapien |
| 2 | 163 | 52.4 | 355 | 1 | Q00182 homo sapien |
| 3 | 41 | 13.2 | 356 | 2 | Q6dk12 homo sapien |
| 4 | 22 | 7.1 | 322 | 2 | Q6P7Q6 rattus norvegicus |
| 5 | 20 | 6.4 | 144 | 1 | P97810 rattus norvegicus |
| 6 | 17 | 5.5 | 323 | 2 | Q6QZP2 canis familiaris |
| 7 | 16 | 5.1 | 317 | 2 | Q9XSM8 sus scrofa |
| 8 | 16 | 5.1 | 349 | 2 | Q9XSM9 sus scrofa |
| 9 | 16 | 4.2 | 322 | 2 | Q99L83 mus musculus |
| 10 | 13 | 4.2 | 353 | 1 | Q08573 mus musculus |
| 11 | 10 | 4.2 | 262 | 2 | P47953 cricetus |
| 12 | 12 | 3.9 | 244 | 1 | Q6PGR5 xenopus laevis |
| 13 | 12 | 3.9 | 261 | 1 | Q08699 rattus norvegicus |
| 14 | 11 | 3.5 | 332 | 2 | Q86G97 xenopus laevis |
| 15 | 11 | 3.5 | 353 | 2 | Q86G97 xenopus laevis |
| 16 | 10 | 3.2 | 262 | 2 | Q90713 gallus gallus |
| 17 | 10 | 3.2 | 296 | 2 | Q9nz03 homo sapien |
| 18 | 10 | 3.2 | 308 | 2 | Q7zTB8 xenopus laevis |
| 19 | 10 | 3.2 | 324 | 1 | P38552 rattus norvegicus |
| 20 | 10 | 3.2 | 328 | 2 | Q86G99 rhipicephalum |
| 21 | 10 | 3.2 | 328 | 2 | Q9tUB8 orcto lagus |
| 22 | 10 | 3.2 | 332 | 2 | Q8QGD9 gallus gallus |
| 23 | 10 | 3.2 | 336 | 1 | LEG3_HUMAN |
| 24 | 9 | 2.9 | 162 | 1 | Q8WN59 ovis aries |
| 25 | 9 | 2.9 | 265 | 2 | Q941Y9 oryza sativa |
| 26 | 9 | 2.9 | 503 | 2 | Q9VPI6 drosophila |
| 27 | 8 | 2.6 | 48 | 2 | Q9QWA2 rattus sp. |
| 28 | 8 | 2.6 | 119 | 2 | Q85FV3 cyanidioschiz |
| 29 | 8 | 2.6 | 121 | 2 | Q86TYS chlorobium |
| 30 | 8 | 2.6 | 122 | 2 | Q8KA12 chlorobium |
| 31 | 8 | 2.6 | 139 | 2 | Q61357 mus musculu |

301 EDITION: THYOT 311

GENESIS 31:1

| RESULT 2 | |
|-----------------------|--|
| DR | EMBL; AB006782; BAA22166.1; -. |
| DR | EMBL; AB005894; BAA3154.1; -. |
| DR | EMBL; AB040130; BAB83625.1; -. |
| DR | EMBL; AB040129; BAB83625.1; JOINED. |
| DR | EMBL; AB040138; BAB83624.1; -. |
| DR | EMBL; AB288083; CAB93851.1; -. |
| DR | EMBL; AB288085; CAB93851.1; JOINED. |
| DR | EMBL; AB288086; CAB93851.1; JOINED. |
| DR | EMBL; AB288087; CAB93851.1; JOINED. |
| DR | EMBL; AB288088; CAB93851.1; JOINED. |
| DR | EMBL; AB288089; CAB93851.1; JOINED. |
| DR | HSSP; P17931; 1A3K. |
| DR | Genew; HGNC:670; LGALS9. |
| DR | MIM: 601879; -. |
| DR | GO; GO:0005530; Fc-galactose binding; TAS. |
| DR | InterPro; IPR008985; Cona-like_lec_g1. |
| DR | InterPro; IPR001079; Galectin. |
| DR | DR PROSITE; PS0037; Gal-bind lectin; 2. |
| DR | DR PROSITE; PS00309; GALAPIN; 2. |
| KW | Alternative splicing; Galectin; Lectin; Repeat. |
| FT | FT DOMAIN 149 206 148 Galactin 1. |
| FT | FT DOMAIN 149 207 149 Linker. |
| FT | FT SITE 82 88 88 Beta-galactoside binding 1 (By similarity). |
| FT | FT SITE 287 293 293 Beta-galactoside binding 2 (By similarity). |
| FT | FT VARPLIC 149 180 Missing (in isoform Short). |
| FT | FT FTID=VSP_003096. |
| FT | FT CONFLICT 5 5 G -> S (in Ref. 3). |
| FT | FT CONFLICT 48 48 N -> D (in Ref. 5). |
| FT | FT CONFLICT 79 81 NGS -> KGR (in Ref. 5). |
| FT | FT CONFLICT 88 88 K -> R (in Ref. 1). |
| FT | FT CONFLICT 89 89 T -> M (in Ref. 5). |
| FT | FT CONFLICT 135 135 S -> F (in Ref. 1). |
| FT | FT CONFLICT 270 270 P -> L (in Ref. 1). |
| FT | FT CONFLICT 313 313 E -> G (in Ref. 1). |
| FT | FT CONFLICT 326 326 L -> V (in Ref. 5). |
| FT | FT CONFLICT 341 341 R -> K (in Ref. 5). |
| SQ | SEQUENCE 355 AA; 3951.8 MW; 4748C22FCFA536A CRC64; |
| Query Match | 52.4%; Score 163; DB 1; Length 355; |
| Best Local Similarity | 100.0%; Pred. No. 1.7e-162; |
| Matches 163; | Conservative 0; Mismatches 0; Indels 0; Gaps 0 |
| Qy | 149 TQTIVHTVOSAPGQNFSTPAIPPMYMPHAYPPMFTTITGLGLYPSKSILLSGTLPVSAQ 208 |
| Db | 193 TQTIVHTVQSAPGQNFSTPAIPPMYMPHAYPPMFTTITGLGLYPSKSILLSGTLPVSAQ 252 |
| Qy | 209 RPHINICSGNHNIAFFHLNPREDENAVYRNTQIDNSNGSEERSLPRKMPFVRGOSFSYWLIC 268 |
| Db | 253 RFHINICSGNHNIAFFHLNPREDENAVYRNTQIDNSNGSEERSLPRKMPFVRGOSFSYWLIC 312 |
| Qy | 269 EAHCUKVADQHLEYYHRLNLPITNRLLEVGGDQLTHYQT 311 |
| Db | 313 EAHCUKVADQHLEYYHRLNLPITNRLLEVGGDQLTHYQT 355 |
| RESULT 3 | |
| ID | Q6DK12 PRELIMINARY; |
| AC | Q6DK12; 28, Created) |
| DT | 25-Oct-2004 (TREMBrel. 28, Last sequence update) |
| DT | 25-Oct-2004 (TREMBrel. 28, Last annotation update) |
| DC | Hypothetical protein. |
| OS | Homo sapiens (Human). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |
| NCBI TaxID | 9606; |
| OX | |

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11

cell membranes, allowing urate that is formed during purine metabolism to efflux from cells and serving as an electrogenic transporter that plays an important role in renal and gastrointestinal urate excretion. Highly selective to the anion urate.

-!- SUBCELLULAR LOCATION: Cytoplasmic. May also be secreted by a non-classical secretory pathway (By similarity).

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Comment=Additional isoforms seem to exist;

Name=Long;

Id=997840-1; Sequence=Displayed;

IsoId=p97840-2; Sequence=VSP 003098;

-!- TISSUE SPECIFICITY: The long form is expressed exclusively in the small intestine. Contains two homologous but distinct carbohydrate-binding domains.

-!- SIMILARITY: Belongs to the galectin (galaptin/s-lectin) family.

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EMBL; US9462; AAB51192.1; -.

EMBL; UT2741; AAB8592.1; -.

EMBL; UT7958; AAB8591.1; -.

HSSP; P17931; 1A3T.

RGD; 3005; Igals9.

InterPro; IPR008995; ConA_like_lec_g1.

InterPro; IPR001019; Galectin.

PFam; PF003337; Gal-bind_lectin.

PROSITE; PS003109; GALAPTIN_2.

DR DOMAIN 1 147 Galaptin 1.

FT DOMAIN 148 205 Linker.

FT DOMAIN 206 354 Galaptin 2.

FT SITE 81 87 Beta-galactoside binding 1 (By similarity).

FT SITE 286 292 Beta-galactoside binding 2 (By similarity).

FT VARSPLIC 148 179 Missing (in isoform Short).

SQ SEQUENCE 354 AA; 39946 MW; /PRID=VSP_003098; RESULT 7

Query Match 7.1%; Score 22; DB 1; Length 354;

Best Local Similarity 100.0%; Prod. No. 4.7e-14; Mismatches 0; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 AVNFGTGFSGNDIAFHFNPRFE 67

Dy 45 AVNFGTGFSGNDIAFHFNPRFE 66

RESULT 6

LEGS_RAT

ID LEGS_RAT; STANDARD; PRT; 144 AA.

AC P41967; 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE Galactin-5 (RL-1B).

GN Name=Lgals5;

OS Rattus norvegicus (Rat).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RA Bannasch D.L., Ryan J.R., Bannasch M.J., Schable R.H., Breen M., Lang G.;

RT "Exclusion of galectin 9 as a candidate gene for hyperuricosuria in the Dalmatian dog";

RL Anim. Genet. 35:26-32 (2004).

CC -!- SIMILARITY: Belongs to the galectin (galaptin/s-lectin) family.

DR EMBL; AY521549; AAS80311.1; -.

DR HSSP; P17931; 1A3T.

GO; GO:0005529; F; sugar binding; IEA.

DR InterPro; IPR008985; ConA_like_lec_g1.

DR InterPro; IPR01019; Galectin.

PFam; PF003337; Gal-bind_lectin; 2.

RN [1]

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

| | | | |
|-----------------------|---|----|---|
| KW | Acetylation; Galectin; IgB-binding protein; Lectin; Phosphorylation; | CC | similarity). |
| KW | Repeat. | CC | -I- SIMILARITY: In the C-terminal section; belongs to the galectin (Galaptin)(S-lectin) family. |
| FT | INIT_MBT | CC | CC |
| FT | SITE_175 | CC | CC |
| FT | MOD_RES_1 | CC | CC |
| FT | MOD_RES_5 | CC | CC |
| FT | DOMAIN_34 | CC | CC |
| FT | REPEAT_34 | CC | CC |
| FT | REPEAT_43 | CC | CC |
| FT | REPEAT_52 | CC | CC |
| FT | REPEAT_61 | CC | CC |
| FT | REPEAT_70 | CC | CC |
| FT | REPEAT_88 | CC | CC |
| FT | DISULFID_DOMAIN_112 | CC | CC |
| SQ | SEQUENCE_244_AA; | CC | CC |
| Query Match | 3.9%; | CC | CC |
| Best Local Similarity | 100.0%; | CC | CC |
| Matches | 12; Conservative 0; Mismatches 0; Indels 0; | CC | CC |
| Qy | 55 GNDIAFHNPFRF 66 | CC | CC |
| Db | 146 GNDIAFHNPFRF 157 | CC | CC |
| RESULT 13 | | CC | CC |
| LEG3_RAT | STANDARD; | CC | CC |
| AC | P08659; ID LEG3_RAT | CC | CC |
| DT | 01-JAN-1998 (Rel.: 06, Created) | CC | CC |
| DT | 01-JUN-1995 (Rel.: 32, Last sequence update) | CC | CC |
| DT | 25-JAN-2005 (Rel.: 46, Last annotation update) | CC | CC |
| DE | Galectin-3 (Galactose-specific lectin 3) (Mac-2 antigen) (IgB-binding protein) (35 kDa lectin) (Carbohydrate binding protein 35) (CBP 35) (Laminin-binding protein) (Lectin L-29). | CC | CC |
| GN | Name=Igals3; | CC | CC |
| OS | Rattus norvegicus (Rat). | CC | CC |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. | CC | CC |
| OX | NCBI_Taxid=10116; | CC | CC |
| RN | [1] | CC | CC |
| RP | SEQUENCE FROM N.A. | CC | CC |
| RP | SEQUENCE OF 124-261 FROM N.A. | CC | CC |
| RP | MEDLINE=88016189; PubMed=1958948; | CC | CC |
| RA | Albrandt K., Orida N.K., Liu F.-T. | CC | CC |
| RT | "An IgB-binding protein with a distinctive repetitive sequence and homology with an IgG receptor."; | CC | CC |
| RL | Proc. Natl. Acad. Sci. U.S.A. 82:4100-4104 (1985). | CC | CC |
| RN | [2] | CC | CC |
| RP | SEQUENCE FROM N.A. | CC | CC |
| RP | SEQUENCE OF 119-144. | CC | CC |
| RP | MEDLINE=90105471; PubMed=2605254; | CC | CC |
| RA | Lefler H., Masiarz P.R., Barondes S.H.; | CC | CC |
| RA | "Soluble lactose-binding vertebrate lectins: a growing family."; | CC | CC |
| RL | Biochemistry 28:9222-9229 (1989). | CC | CC |
| RN | [3] | CC | CC |
| RP | SEQUENCE FROM N.A. | CC | CC |
| RP | SEQUENCE OF 124-261 FROM N.A. | CC | CC |
| RA | Liu F.-T., Albrandt K., Mendel E., Kulczycki A. Jr., Orida N.K.; | CC | CC |
| RT | "Identification of an IgB-binding protein by molecular cloning."; | CC | CC |
| RL | Proc. Natl. Acad. Sci. U.S.A. 82:4100-4104 (1985). | CC | CC |
| RN | [4] | CC | CC |
| RP | SEQUENCE FROM N.A. | CC | CC |
| RP | SEQUENCE, AND ACETYLATION. | CC | CC |
| RP | MEDLINE=94075368; PubMed=8253005; | CC | CC |
| RA | Hermann J., Thirck C.W., Atchison R.E., Huflejt M.E., Poulter L., | CC | CC |
| RA | Gitt M.A., Burlingame A.L., Barondes S.H., Lefler H.; | CC | CC |
| RT | "Primary structure of the soluble lactose binding lectin L-29 from rat and dog and interaction of its non-collagenous proline-, glycine-, tyrosine-rich sequence with bacterial and tissue collagenase."; | CC | CC |
| RT | J. Biol. Chem. 268:26704-26711 (1993). | CC | CC |
| CC | "Purification and cDNA cloning of Xenopus liver galectins and their expression."; | CC | CC |
| CC | -I- SUBUNIT: Probably forms homo- or heterodimers. Binds IgE. | CC | CC |
| CC | -I- FUNCTION: Galactose-specific lectin which binds IgE. | CC | CC |
| CC | -I- EXPRESSION: Purification and cDNA cloning of Xenopus liver galectins and their expression."; | CC | CC |
| RESULT 14 | | CC | CC |
| OBUNW97 | OBUNW97 | CC | CC |
| AC | OBUNW97; | CC | CC |
| DT | 01-MAR-2002 (T-EMBLrel. 20, Created) | CC | CC |
| DT | 01-MAR-2002 (T-EMBLrel. 20, Last sequence update) | CC | CC |
| DT | 01-MAR-2004 (T-EMBLrel. 26, Last annotation update) | CC | CC |
| DE | Galectin family_xgalectin-IVa. | CC | CC |
| GN | Xenopus laevis (African clawed frog). | CC | CC |
| OS | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Xenopus laevis (African clawed frog). | CC | CC |
| OC | Xenopidae; Batrachia; Anura; Mesobatrachia; Pipidae; | CC | CC |
| OC | Xenopodinae; Xenopus. | CC | CC |
| OC | NCBI_TaxID=8355; | CC | CC |
| OX | | CC | CC |
| RN | SEQUENCE FROM N.A. | CC | CC |
| RP | SEQUENCE OF 124-261 FROM N.A. | CC | CC |
| RA | Albrandt K., Mendel E., Kulczycki A. Jr., Orida N.K.; | CC | CC |
| RT | "Identification of an IgB-binding protein by molecular cloning."; | CC | CC |
| RL | Proc. Natl. Acad. Sci. U.S.A. 82:4100-4104 (1985). | CC | CC |
| RN | [1] | CC | CC |
| RP | SEQUENCE OF 119-144. | CC | CC |
| RP | MEDLINE=90105471; PubMed=2605254; | CC | CC |
| RA | Lefler H., Masiarz P.R., Barondes S.H.; | CC | CC |
| RA | "Soluble lactose-binding vertebrate lectins: a growing family."; | CC | CC |
| RL | Biochemistry 28:9222-9229 (1989). | CC | CC |
| RN | [2] | CC | CC |
| RP | SEQUENCE, AND ACETYLATION. | CC | CC |
| RP | MEDLINE=94075368; PubMed=8253005; | CC | CC |
| RA | Hermann J., Thirck C.W., Atchison R.E., Huflejt M.E., Poulter L., | CC | CC |
| RA | Gitt M.A., Burlingame A.L., Barondes S.H., Lefler H.; | CC | CC |
| RT | "Primary structure of the soluble lactose binding lectin L-29 from rat and dog and interaction of its non-collagenous proline-, glycine-, tyrosine-rich sequence with bacterial and tissue collagenase."; | CC | CC |
| RT | J. Biol. Chem. 268:26704-26711 (1993). | CC | CC |
| CC | "Purification and cDNA cloning of Xenopus liver galectins and their expression."; | CC | CC |

RL Glycobiology 12:163-172 (2002).
 CC -1- SIMILARITY: Belongs to the galectin (galaptin/S-lectin) family.
 EMBL: AB060972; BAB83259.1; -.
 DR HSSP; P17931; 1A3K.
 DR GO:000972; F:sugar binding; IEA.
 DR GO; GO:005529; F:sugar binding; IEA.
 DR Pfam; PF00337; Gal-bind lectin; 2.
 SMART; SM00276; GLECT; 2.
 DR Lectin; Lectin.
 KW SEQUENCE: 332 AA; 36822 MW; D273FB035484E9C2 CRC64;
 SQ DR HSSP; P17931; 1A3K.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR InterPro; IPR008985; ConA-like_lec_g1.
 DR InterPro; IPR001019; Galactin.
 DR Pfam; PF00337; Gal-bind lectin; 2.
 DR SMART; SM00276; GLECT; 2.
 KW Galactin; Lectin.
 FT NON_TER 1 1
 SQ SEQUENCE 353 AA; 39242 MW; 0453CD4E93DB1C6 CRC64;
 DR Query Match 3.5%; Score 11; DB 2; Length 353;
 DR Best Local Similarity 100.0%; Pred. No. 0.017; No. 0.018;
 DR Matches 11; Conservative 0; Mismatches 0; Gaps 0;
 DR Indels 0;
 DR QY 56 NDIAFHENPRF 66
 DR ||||| |||||
 DR 50 NDIAFHENPRF 60
 DR ||||| |||||
 DR Db 71 NDIAFHENPRF 81

RESULT 15
 Q6PGR5 PRELIMINARY ;
 ID Q6PGR5 PRELIMINARY ;
 AC PRT; 353 AA.
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Xgalectin-iva Protein (Fragment).
 CN Name=xgalectin-iva.
 OS Xenopus laevis (African clawed frog).
 EUkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 OC Xenopodinae; Xenopidae.
 OX NCBI_TaxID=8355;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Feingold E.A., Grouse L.H., Degege J.G., Schaefer C.F., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Ronald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Osdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,
 RA Bossak S.A., McEwan P.J., McFernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faley J., Heitton B., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Shalska U., Smailus D.E., Schnierch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.I., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391 (2002).
 RN [3]

RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA Klein S., Strausberg R.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the galectin (galaptin/S-lectin) family.
 DR EMBL; BC056859; AAH56859.1; -.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 13, 2005, 07:46:47 ; Search time 163 Seconds

Title: US-09-263-689-4

Perfect score: 311

Sequence: 1 MAFSGSQAPYLSPAVPPSGT.....LPTINRLEVGGDIQIQLTHVQT 311

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: GeneseqP1980:*

2: GeneseqP1990:*

3: GeneseqP2000:*

4: GeneseqP2001:*

5: GeneseqP2002:*

6: GeneseqP2003:*

7: GeneseqP2003b:*

8: GeneseqP2004:*

RESULT 1
AAW55504

ID AAW55504 standard; protein; 311 AA.

XX

AC AAW55504;

XX

DT 14-SPR-1998 (first entry)

XX

DE Human galectin 9.

XX

KW Galactin 9; lectin; human; autoimmune disease; inflammatory disease; Hodgkin disease; asthma; allergy; melanoma; renal astrocytoma; bone cancer; liver cancer; breast cancer; ovarian cancer; prostate cancer; bone cancer; diagnosis; therapy; lung cancer; pancreas cancer; spleen cancer; diagnosis; therapy.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-----------------|---------------------|
| 1 | 311 | 100.0 | 311 2 AAW55504 | Aaw55504 Human gal |
| 2 | 306 | 98.4 | 311 2 ABB77854 | Abb77854 Amino aci |
| 3 | 163 | 52.4 | 233 8 ADP81097 | Adp81097 Protein O |
| 4 | 163 | 52.4 | 323 3 AY56802 | Aay56802 Human eos |
| 5 | 163 | 52.4 | 323 5 ABB77853 | Abb77853 Amino aci |
| 6 | 163 | 52.4 | 323 5 ABP61494 | Abp61494 Human NF- |
| 7 | 163 | 52.4 | 323 8 ADQ66730 | Adq66730 Novel hum |
| 8 | 163 | 52.4 | 355 2 AAY06937 | Aay06937 Galectin- |
| 9 | 163 | 52.4 | 355 2 AAW85664 | Aaw85664 Galectin- |
| 10 | 163 | 52.4 | 355 5 ABB77852 | Abb77852 Amino aci |
| 11 | 163 | 52.4 | 355 7 ADC53845 | Adc53845 Human gal |
| 12 | 163 | 52.4 | 355 7 ADE62929 | Ad62929 Human Pro |
| 13 | 163 | 52.4 | 355 7 ADD48101 | Add48101 Human Pro |
| 14 | 163 | 52.4 | 355 7 ADGG91608 | Adgg91608 Human lec |
| 15 | 163 | 52.4 | 378 4 AAE13847 | Aae13847 Human lun |
| 16 | 163 | 52.4 | 378 5 ADD66747 | Add66747 Human lun |
| 17 | 163 | 52.4 | 378 7 ADE88001 | Ades88001 Human lun |
| 18 | 148 | 47.6 | 168 3 AAB11899 | Aab11899 Human col |
| 19 | 148 | 47.6 | 168 4 Aam24496 | Aam24496 Colon tum |
| 20 | 148 | 47.6 | 168 6 ABP55345 | Abp55345 Human col |
| 21 | 148 | 47.6 | 301 7 ABU63651 | Abu63651 Human ura |
| 22 | 87 | 28.0 | 323 8 ADP12958 | Adp12958 Protein e |
| 23 | 73 | 23.5 | 246 5 ABU69164 | Abu69164 Human NOV |
| 24 | 73 | 23.5 | 246 8 ADO08331 | Ado08331 Human NOV |
| 25 | 69 | 22.2 | 145 2 Aaw61613 | Aaw61613 Human gal |

ALIGNMENTS

Claim 9; Fig 2A-B; 118PP; English.
This polypeptide comprises novel human galectin 9. Its amino acid

CC

CC sequence was deduced from a human adult pancreatic tumour cDNA clone (see
 CC AA597851). Novel galectins 8, 9, 10 and 10Sv variant (10Sv) are
 CC claimed (see AA55503-06). These can be obtained using a claimed method
 CC by expression in recombinant host cells. The novel galectins are used in
 CC a claimed method for treating a cell growth disorder, especially cancer,
 CC autoimmune diseases, inflammatory diseases, asthma, and allergic
 CC diseases, in a mammal. They are especially useful for diagnosis of
 CC melanoma, renal astrocytoma, Hodgin's disease, and breast, ovarian,
 CC prostate, bone, liver, lung, pancreatic and splenic cancers; The
 CC invention further relates to screening methods for identifying agonists
 CC and antagonists of galectin 8, 9, 20 or 10Sv activity, and to diagnostic
 CC methods involving estimating levels of galectin 8, 9, 10 or 10Sv protein
 CC or mRNA

XX Sequence 311 AA;
 SQ Score 311; DB 2; Length 311;
 Best Local Similarity 100.0%; Pred. No. 4.1e-305;
 Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFSGSOAIPYLSPAVPFSGSTIOGGHQDGQIQTGVTLVSSSGTRPFAVNQFOTGFSGNDIAF 60
 Db 1 MAFSSQAOAIPYLSPAVPFSGTIGQHQDGQIQTGVTLVSSSGTRPFAVNQFOTGFSGNDIAF 60

QY 61 HENPREFEDGQYVVCNTROGSWGPBEEKTHMPFKGMPFDLCLFVQSSDFKVNNGILFV 120
 Db 61 HENPREFEDGQYVVCNTROGSWGPBEEKTHMPFKGMPFDLCLFVQSSDFKVNNGILFV 120

QY 121 QYFHRRVPFRVDTISVNGSVQLSYSTISFOTOTVHTVQSGQMFSTPA1PPMMYPHPAVP 180
 Db 121 QYFHRRVPFRVDTISVNGSVQLSYSTISFOTOTVHTVQSGQMFSTPA1PPMMYPHPAVP 180

QY 181 MPFITTIGGLYPSKSILLSGTVPSSAQRFHNLNPRDENAVVRNTQD 240
 Db 181 MPFITTIGGLYPSKSILLSGTVPSSAQRFHNLNPRDENAVVRNTQD 240

QY 241 NSWGBEERSLPRKMPFVRGQSFSTWILCRAHCLKVADQQLPEYYHRNLPTINRLEY 300
 Db 241 NSWGBEERSLPRKMPFVRGQSFSTWILCRAHCLKVADQQLPEYYHRNLPTINRLEY 300

QY 301 GDDIQLTHYQT 311
 Db 301 GDDIQLTHYQT 311

RESULT 2
 ID ABB77854 standard; protein; 311 AA.

XX ABB77854;
 XX 27-SEP-2002 (first entry)

XX Amino acid sequence of a human protein.

XX Cancer; galectin 9; antibody; skin cancer; melanoma; breast cancer;
 KW ovarian cancer; uterus cancer; tumour; prostate cancer; bladder cancer;
 KW kidney cancer; thyroid cancer; throat cancer; tongue cancer;
 KW upper jaw cancer; esophageal cancer; stomach cancer;
 KW lung cancer; liver cancer; gall-bladder cancer; pancreatic cancer;
 KW leukemia; liposarcoma; glioma.
 OS Homo sapiens.
 XX WO200237114-A1.
 XX PR 10-MAY-2002.
 XX 31-OCT-2001; 2001WO-JP009561.
 XX PR 01-NOV-2000; 2000JP-00335077.
 PA (GALP-) GALPHARMA CO LTD.

| | |
|-------------------------|---|
| XX | Hirashima M, Yamauchi A, Kagesita T, Nakamura T, Nishi N; |
| PI | |
| DR | WPI; 2002-519265/55. |
| XX | Metastasis mechanism-based agents (anti-galectin 9 antibody) for PT detecting ability of cancer to metastasize in cells, uses galectin 9 as PT marker to detect cancer metastasis for diagnosis, cancer prevention and PT treatment. |
| XX | Disclosure; Page 63-64; 68pp; Japanese. |
| PS | |
| XX | The specification describes an agent for detecting the ability of cancers CC to metastasize. This agent comprises anti-galectin 9 antibody as the active ingredient. The agents and method are for or detecting ability of CC cancer to metastasize in cancer cells, which are useful in the diagnosis, prevention and treatment of cancer. The cancer includes epithelial CC malignant tumours (tumourising or non-tumourising) in organs, tissues or blood. Such cancer can be 1 of the not less than 31 specifically claimed, e.g. skin cancer (including melanoma), breast cancer, ovarian cancer, CC uterus cancer, malignant tumour of the testis, prostate cancer, bladder cancer, kidney cancer, thyroid cancer, cancer of throat and larynx, CC tongue cancer, upper jaw cancer, esophageal cancer, stomach cancer, colon and rectum cancer, lung and bronchus cancer, liver cancer (including CC hepatocarcinoma and intrahepatic biliary cancer), extrahepatic biliary CC duct and gall-bladder cancer, pancreatic cancer, leukemia, malignant CC lymphoma, liposarcoma and glioma. The cancer cells are particularly CC breast cancer cells or melanoma cells. The present sequence represents a CC human protein, which is used in the course of the invention |
| XX | Sequence 311 AA; |
| SQ | |
| Query Match | 98.4%; Score 306; DB 5; Length 311; |
| Best Local Similarity | 100.0%; Pred. No. 4.6e-300; |
| Matches | 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| QY | |
| Db | |
| QY | 6 SQAPYLSPAPPFSTIOGLQDGQIQTGVTLVSSSGTRPFAVNQFOTGFSGNDIAFHENP 65 Db 6 SQAPYLSPAPPFSTIOGLQDGQIQTGVTLVSSSGTRPFAVNQFOTGFSGNDIAFHENP 65 |
| QY | 66 FEDGGVVCNTROGSWGPBEEKTHMPFKGMPFDLCLFVQSSDFKVNNGILFVQYFHR 125 Db 66 FEDGGVVCNTROGSWGPBEEKTHMPFKGMPFDLCLFVQSSDFKVNNGILFVQYFHR 125 |
| QY | 126 VPFFRVDITISVNGSVQLSYSTISFOTOTVHTVQSGQMFSTPA1PPMMYPHPAVPPT 185 Db 126 VPFFRVDITISVNGSVQLSYISFOTOTVHTVQSGQMFSTPA1PPMMYPHPAVPPT 185 |
| QY | 186 TIGGGLYPSKSILLSGTVPSSAQRFHNLNPRDENAVVRNTQD 245 Db 186 TIGGGLYPSKSILLSGTVPSSAQRFHNLNPRDENAVVRNTQD 245 |
| QY | 187 TIGGGLYPSKSILLSGTVPSSAQRFHNLNPRDENAVVRNTQD 245 Db 187 TIGGGLYPSKSILLSGTVPSSAQRFHNLNPRDENAVVRNTQD 245 |
| QY | 246 EERSLPRKMPFVRGQSFSTWILCRAHCLKVADQQLPEYYHRNLPTINRLEY 305 Db 246 EERSLPRKMPFVRGQSFSTWILCRAHCLKVADQQLPEYYHRNLPTINRLEY 305 |
| QY | 306 LTHYQT 311 Db 306 LTHYQT 311 |
| RESULT 3 ID ADP81097 | |
| XX | ADP81097 standard; protein; 233 AA. |
| AC | |
| XX | 09-SEP-2004 (first entry) |
| DE | Protein of human ovarian specific gene, SEQ ID No 131. |
| XX | normal; neoplastic; ovarian; specific nucleic acid; OSNA; |
| KW | metastatic; cancer; vaccine; cytostatic; human. |
| PA | |

| | | | | | |
|----|---|----------------------|--|--|--|
| XX | Homo sapiens. | | | | |
| OS | WO200405079-A2. | | | | |
| PN | 24-JUN-2004. | | | | |
| XX | PD | WPI; 2004-468850/44. | | | |
| XX | PF | DR; ADP80368. | | | |
| XX | 08-DEC-2003; 2003WO-US038855. | | | | |
| PR | 06-DBC-2002; 2002US-0431301P. | | | | |
| PR | 06-DBC-2002; 2002US-0431321P. | | | | |
| PR | 30-JUN-2003; 2003US-048584P. | | | | |
| PR | 07-NOV-2003; 2003US-0518607P. | | | | |
| XX | (DIAD-) DIADEXUS INC. | | | | |
| XX | Macina RA, Turner LR, Sun Y, Liu S, Chen H; | | | | |
| XX | WPI; 2004-468850/44. | | | | |
| XX | DR; ADP80368. | | | | |
| XX | New ovarian specific nucleic acid molecules and polypeptides useful for diagnosing, preventing or treating ovarian cancer, for producing transgenic animals or cells, or for research purposes. | | | | |
| PT | PT | XX | | | |
| PT | Claim 12; SEQ ID NO 131; 754pp; English. | | | | |
| PS | XX | | | | |
| CC | The invention relates to novel isolated nucleic acid molecules and polypeptides present in normal and neoplastic ovarian cells. These comprise a nucleic acid sequence encoding any of the 167 amino acid sequences (e.g. 43, 237 or 233 amino acids) fully defined in the specification (SEQ ID NOS: ADP81095 to ADP81261) and comprises any of the 128 nucleotide sequences (e.g. 4798, 1494 or 1691 bp) fully defined in the specification (SEQ ID NOS: ADP80967 to ADP81094). The invention further comprises: a method for determining the presence of a ovarian specific nucleic acid (OSNA) in a sample; a vector comprising the above nucleic acid molecule; a host cell comprising the vector; a method for producing a polypeptide encoded by the above nucleic acid molecule; a polypeptide encoded by the nucleic acid molecule cited above; an antibody or its fragment that specifically binds to the above polypeptide; a method for determining the presence of an ovarian specific protein in a sample; a method for diagnosing or monitoring the presence and metastases of ovarian cancer in a patient; a kit for detecting a risk of cancer or presence of cancer in a patient, the kit comprising a means for determining the presence of the above nucleic acid molecule or polypeptide; a method of treating a patient with ovarian cancer; and a vaccine comprising the above polypeptide or nucleic acid encoding the polypeptide. The isolated nucleic acid molecules and polypeptides have cytostatic activity. The isolated polypeptides may be used to create a vaccine. The isolated nucleic acid molecules and polypeptides can be used for diagnosing or monitoring the presence and metastases of ovarian cancer and treating ovarian cancer. This sequence represents the protein of an ovarian specific gene of the invention. | | | | |
| CC | Sequence 233 AA; | | | | |
| CC | Score 163; DB 8; Length 233; | | | | |
| CC | Best Local Similarity 100.0%; Pred. No. 8.7e-156; | | | | |
| CC | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | |
| Qy | 149 TQTVTHYQSAQGMFSTPAIPPMYPPAYPMFPTTILGGLYPSKSILLSGTVPSSWILC 268 | | | | |
| Db | 71 TQTVTHYQSAQGMFSTPAIPPMYPPAYPMFPTTILGGLYPSKSILLSGTVPSSWILC 130 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 311 | | | | |
| Db | 191 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGDQLQTHVQT 233 | | | | |
| Qy | 209 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 268 | | | | |
| Db | 131 RPHINLCSGNHIAFHLPNRFDENAVRNTQIDNSMGSEERSLPRKMPFTRGQSFSWILC 190 | | | | |
| Qy | 269 EAHCLKVAVGQHLPFEYHRLNLPFTINRLEVGGD | | | | |

Page 4

Amino acid sequence of a human protein.

DE XX Cancer; galectin 9; antibody; skin cancer; melanoma; breast cancer; ovarian cancer; uterus cancer; tumour; prostate cancer; bladder cancer; kidney cancer; thyroid cancer; throat cancer; tongue cancer; upper jaw cancer; esophageal cancer; stomach cancer; colon cancer; lung cancer; liver cancer; gall-bladder cancer; pancreatic cancer; leukemia; liposarcoma; glioma.

XX OS Homo sapiens.

XX PN WO200237114-A1.

XX PD 10-MAY-2002.

XX PF 31-OCT-2001; 2001WO-JP009561.

XX PR 01-NOV-2000; 2000JP-00335077.

XX PA (GALP-) GALPHARMA CO LTD.

XX PI Hirashima M, Yamauchi A, Kageshita T, Nakamura T, Nishi N;

XX DR WPI; 2002-519265/55.

XX PS Example 5; Page 61-63; 68pp; Japanese.

XX The specification describes an agent for detecting the ability of cancer to metastasize. This agent comprises anti-galectin 9 antibody as the active ingredient. The agents and method are for or detecting ability of cancer to metastasize in cancer cells, which are useful in the diagnosis prevention and treatment of cancer. The cancer includes epithelial malignant tumours (tumourising or non tumourising) in organs, tissues or blood. Such cancer can be 1 of the not less than 31 specifically claimed e.g. skin cancer (including melanoma), breast cancer, ovarian cancer, uterus cancer, malignant tumour of the testis, prostate cancer, bladder cancer, kidney cancer, thyroid cancer, cancer of throat and larynx, tongue cancer, upper jaw cancer, esophageal cancer, stomach cancer, colon and rectum cancer, lung and bronchus cancer, liver cancer (including hepatocarcinoma and intrahepatic biliary cancer), extrahepatic biliary duct and gall-bladder cancer, pancreatic cancer, leukemia, malignant lymphoma, liposarcoma and glioma. The cancer cells are particularly human in origin, which is used in the course of the invention.

XX CC The present sequence represents a

| | | | |
|---------|------------------|--|----------------------------------|
| XX | 5Q | Sequence | 323 AA; |
| Query | Match | 52.4% | Score 163; DB 5; Length 323; |
| Best | Local Similarity | 100.0% | Pred. No. 1.e-15; |
| Matches | Matches | 163 | No. Mismatches 0; Indels 0; Gaps |
| Qy | 149 | TQVTHYQSAPGMFSTPAIPPMYPAIPMFITTLGGLYPSKSILLSGTVLPSAQ | 21 |
| Db | 161 | TQVTHYQSAPGMFSTPAIPPMYPAIPMFITTLGGLYPSKSILLSGTVLPSAQ | 21 |
| Qy | 209 | RFFINLCSGNHIAFHLPFRDENAVVRNQTIDNSWGSEERSLPRKMPFVRGQFSFSWVILC | 26 |
| Db | 221 | RFFINLCSGNHIAFHLPFRDENAVVRNQTIDNSWGSEERSLPRKMPFVRGQFSFSWVILC | 26 |
| Qy | 269 | EAIICLKVAVDGQHIFFEYTHRLNPTINRLEVGDIQIOTHVQT | 311 |
| Db | 281 | PAICLKVADGQHIFFEYTHRLNPTINRLEVGDIQIOTHVQT | 323 |

| | |
|-------------------------------|---|
| AC | ABP61494; |
| XX | |
| DT | 30-SEP-2002 (first entry) |
| XX | Human NF- κ B activating protein SEQ ID NO 141. |
| DE | |
| KW | Human; NF- κ B; nuclear factor kappa B; mouse; antiinflammatory; |
| KW | immunomodulator; cytotoxic; antiinfective; osteopathic; nootropic; |
| KW | neuroprotective; anti HIV; autoimmune disease; cancer; infection; |
| KW | bone disease; AIDS; neurodegenerative disease; ischaemic disorder |
| XX | |
| OS | <i>Homo sapiens</i> . |
| XX | |
| PN | WO20025737-A1. |
| XX | |
| PD | 11-JUL-2002. |
| XX | |
| PP | 2001WO-JP011389. |
| XX | |
| PR | 28-DEC-2000; 20000JP-00402288. |
| PR | 26-MAR-2001; 2001JP-0008912. |
| PR | 24-AUG-2001; 2001JP-00254018. |
| XX | |
| (ASAH) ASAHI KASEI KOGYO KK. | |
| PA | |
| XX | Matuda A, Honda G, Muramatsu S, Nagano Y; |
| PI | |
| XX | |
| WPI; | 2002-583617/62. |
| DR | N-2SDB; ABO91982. |
| XX | |
| PT | NF- κ B activating gene and expressed protein, applical |
| PT | diagnosis and screening inhibitors or promoters to control excess |
| PT | activation or inhibition for treating e.g. inflammations, autoimmu |
| PT | nisms and cancer. |
| XX | |
| PS | Claim 1; Page 613-615; 841pp; Japanese. |
| XX | |
| CC | The invention relates to a purified protein (I), comprising one or |
| CC | fully defined sequences (AB6144-AB6151) or a protein based on |
| CC | the sequences but with some amino acids deleted, substituted or ac |
| CC | with a NF- κ B (nuclear factor kappa B) activating effect. The prote |
| CC | in coding gene (AB091912-AB092001) are useful in diagnosis and scri |
| CC | inhibitors or promoters to control excessive activation or inhibi |
| CC | for treating e.g. inflammations, autoimmune diseases, cancers, |
| CC | infections, bone diseases, AIDS, neurodegenerative diseases or is |
| CC | disorders |
| XX | |
| SQ | Sequence 323 AA; |

| Query | Match | Score | DB | Length |
|-------|-----------------------|--|------------|---------------|
| dy | Best Local Similarity | 52.4† | 163; | DB 5; |
| | Matches | 100.0† | Pred. | No. 1.2e-155; |
| dy | Conservative | 0; | Mismatches | 0; |
| dy | Matches | 163; | Indels | 0; |
| dy | | | Gaps | 0; |
| dy | 149 | TQTVIHTVQSACQMFSTPAIPMMYPPAYPMPPFITLIGGLYPSKSILLSGTVLPSAQ | 208 | |
| dy | 161 | TQTVIHTVQSACQMFSTPAIPMMYPPAYPMPPFITLIGGLYPSKSILLSGTVLPSAQ | 220 | |
| dy | 209 | RPHINLCSGNHIAFHLMNPREFDENAVRVTQIDNSWGSEERSLPRKMPFVRGQSFSWILC | 268 | |
| dy | 221 | RPHINLCSGNHIAFHLMNPREFDENAVRVTQIDNSWGSEERSLPRKMPFVRGQSFSWILC | 280 | |
| dy | 269 | EAHCLKVAVDGQLFEYTHRLNLUPTIRLEVGDIQLTHVQT | 311 | |
| dy | 281 | EAHCLKVAVDGQLFEYTHRLNLUPTIRLEVGDIQLTHVQT | 323 | |

RESULT 6
ABP61494 ABP61494 standard; protein; 323 AA.

ADDQ66730 ID: ADDQ66730 standard; protein; 323 AA.
XX
AC
XX
ADDQ66730;
XX
07-OCT-2004 (First entry)

| | | | |
|----|---|--|---|
| XX | Novel human protein sequence #1703. | KW | prostate cancer. |
| XX | | XX | Homo sapiens. |
| KW | osteoprotective; nootropic; anti parkinsonian; cytosatic; | XX | |
| KW | gene therapy; diagnostic marker; morbid state; osteoporosis; | XX | |
| KW | neurological disease; Alzheimer's disease; Parkinson's disease; dementia; | XX | |
| XX | cancer. | XX | |
| OS | Homo sapiens. | XX | |
| XX | | XX | |
| PN | EP1440981-A2. | PR | 17-JUL-1997; 97US-00896164. |
| XX | | PR | 10-OCT-1997; 97US-0061599P. |
| PD | 28-JUL-2004. | PR | 10-OCT-1997; 97US-0061765P. |
| XX | | PR | 10-OCT-1997; 97US-0098705. |
| PP | 21-JAN-2004; 2004EP-00001196. | PR | 11-OCT-1997; 97GB-0021697. |
| XX | | PR | 22-JUN-1998; 98US-00102322. |
| PR | 21-JAN-2003; 2003JP-00102206. | XX | |
| PR | 09-MAY-2003; 2003JP-00131392. | PA | (LUDWIG) LUDWIG INST CANCER RES. |
| XX | | XX | |
| PA | (REAS-) RES ASSOC BIOTECHNOLOGY. | PI | Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I; |
| XX | | PI | O'hare M, Obata Y, Pfreundschuh M, Tureci O, Sahin U; |
| PI | Isogai T, Sugiyama T, Otsuki T, Wakanatsu A, Sato H, Ishii S; | XX | |
| PI | Yamamoto J, Isono Y, Nagai K, Irie R; | DR | WPI; 1999-132448/11. |
| XX | | DR | N-PSDB; AAX40398. |
| DR | WPI; 2004-535376/52. | XX | |
| XX | | PT | New isolated cancer associated nucleic acids and polypeptides - isolated |
| PT | PT | PT | using sera from cancer patients, used to develop products for the |
| PS | PT | PT | diagnosis, monitoring or treatment of cancers. |
| PS | PS | XX | Example 8; Page 779-780; 787bp; English. |
| XX | | XX | |
| PT | PT | CC | The invention relates to a method for diagnosing a disorder characterised |
| PS | PS | CC | by expression of a human cancer associated antigen precursor coded for by |
| PS | PS | CC | a nucleic acid molecule (NAM). The method comprises: (a) contacting a |
| PS | PS | CC | biological sample isolated from a subject with an agent that specifically |
| PS | PS | CC | binds to the NAM, an expression product or a fragment of an expression |
| PS | PS | CC | product complexed with an HLA molecule; and (b) determining the |
| PS | PS | CC | interaction between the agent and the NAM or the expression product as a |
| PS | PS | CC | determination of the disorder. The products and methods can be used in |
| PS | PS | CC | the diagnosis, monitoring, research, or treatment of conditions |
| PS | PS | CC | characterised by the expression of various cancer associated antigens. |
| PS | PS | CC | The invention provides nucleic acid sequences and encoded polypeptides |
| PS | PS | CC | which are cancer associated antigen precursors expressed in human breast |
| PS | PS | CC | cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and |
| PS | PS | CC | lung cancer. |
| XX | | XX | Sequence 355 AA; |
| XX | | Query Match | 52.4%; Score 163; DB 2; Length 355; |
| XX | | Best Local Similarity | 100.0%; Pred. No. 1.2e-155; |
| XX | | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| XX | | Query | 149 TQTVIHTVQSAPGMFSTPAIPPMYPHAPYPMFITTIGGLYPSKSILLSGTVLPSAQ 208 |
| Db | 161 TQTVIHTVQSAPGMFSTPAIPPMYPHAPYPMFITTIGGLYPSKSILLSGTVLPSAQ 220 | Db | 149 TQTVIHTVQSAPGMFSTPAIPPMYPHAPYPMFITTIGGLYPSKSILLSGTVLPSAQ 208 |
| Db | 161 TQTVIHTVQSAPGMFSTPAIPPMYPHAPYPMFITTIGGLYPSKSILLSGTVLPSAQ 220 | Db | 193 TQTVIHTVQSAPGMFSTPAIPPMYPHAPYPMFITTIGGLYPSKSILLSGTVLPSAQ 252 |
| Qy | 209 RFHINLCSGNHIAFHINPFRDENAVVRNTQIDNSWGSERSLPRKMPFVRGQSFVWILC 268 | Qy | 209 RFHINLCSGNHIAFHINPFRDENAVVRNTQIDNSWGSERSLPRKMPFVRGQSFVWILC 268 |
| Db | 221 RFHINLCSGNHIAFHINPFRDENAVVRNTQIDNSWGSERSLPRKMPFVRGQSFVWILC 280 | Db | 253 RFHINLCSGNHIAFHINPFRDENAVVRNTQIDNSWGSERSLPRKMPFVRGQSFVWILC 312 |
| Qy | 269 EAHCLKVAVDQQLFYYHLRNLPTINRLEVGGDIQLTHVQT 311 | Qy | 269 EAHCLKVAVDQQLFYYHLRNLPTINRLEVGGDIQLTHVQT 311 |
| Db | 281 EAHCLKVAVDQQLFYYHLRNLPTINRLEVGGDIQLTHVQT 323 | Db | 313 EAHCLKVAVDQQLFYYHLRNLPTINRLEVGGDIQLTHVQT 355 |
| XX | | RESULT 8 | |
| XX | | ID AAY06997 standard; protein; 355 AA. | |
| AC | AAV06997; | XX | |
| XX | 02-JUL-1999 (First entry) | XX | |
| DE | Galectin-9 protein sequence. | XX | |
| KW | Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer; | XX | |

DE Galectin 9 like protein.
 XX Galectin-9; lectin; galactose; Hodgkin's disease; pharmaceutical;
 sugar chain; intercellular adhesion; cell proliferation.
 XX OS Homo sapiens.
 XX PN WO9910490-A1.
 XX PD 04-MAR-1999.
 XX PF 19-AUG-1998; 98WO-JP003670.
 XX PR 22-AUG-1997; 97JP-00226468.
 XX PA (SAGA) SAGAMI CHEM RES CENTRE.
 (PROT-) PROTEGENE INC.
 PI Kato S, Yamaguchi T, Sekine S, Kamata K;
 DR 1999-228913/19.
 XX N-PSDB; AAX08490, AAX08491.
 PT A new human protein having lactose binding properties.
 XX PS Claim 2; Page 55-57; 64pp; English.

CC Galactins are the general term for animal lectins binding to galactose.
 CC Lectins exist in many sites such as the cytoplasm, the nucleus,
 CC the cell membrane etc. and are considered to be associated with cell
 CC proliferation. Galactin 9 has been identified as an antigenic protein
 CC reacting with an antibody contained in the serum of Hodgkin's disease and
 CC has a structure where two sugar chain-binding domains are connected by a
 CC linker peptide. The true role of Galactin-9 in the body has not been
 CC completely identified but is thought to be involved in intercellular
 CC adhesion. The human galectin-9 like protein coding sequences are
 CC characterised by containing the sequence described in AAX08489. The
 CC protein can be used as pharmaceuticals or reagents for sugar chain
 CC research. The cDNA is used as a probe for gene diagnosis and for gene
 CC therapy.
 XX Sequence 355 AA;

Query Match 52.4%; Score 163; DB 2; Length 355;
 Best Local Similarity 100.0%; Pred. No. 1.3e-155;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Query 149 TQTVIHTYQOSAPGMFSTPAIPPMYPHPAYPMFPTTLLGGLYPSKSILLSGTVPSSAQ 208
 Db 193 TQTVIHTYQOSAPGMFSTPAIPPMYPHPAYPMFPTTLLGGLYPSKSILLSGTVPSSAQ 252
 Query 209 RFHINLCSGNHIAFHINPREDENAVRNTQIDNSWGSERSLSPRKMPFTRGQSFVWILC 268
 Db 253 RFHINLCSGNHIAFHINPREDENAVRNTQIDNSWGSERSLSPRKMPFTRGQSFVWILC 312
 Query 269 EAHCILKVAVDGQHLPFYYHLRNLPTINLEVGDIQLTHVQT 311
 Db 313 EAHCILKVAVDGQHLPFYYHLRNLPTINLEVGDIQLTHVQT 355
 RESULT 10
 ID ABB7852 standard; protein; 355 AA.
 XX ABB7852;
 XX DT 27-SEP-2002 (first entry)
 DE Amino acid sequence of a human protein.
 XX Cancer; galectin 9; antibody; skin cancer; melanoma; breast cancer;
 KW ovarian cancer; uterus cancer; tumour; prostate cancer; bladder cancer;
 KW kidney cancer; thyroid cancer; throat cancer; tongue cancer;

KW upper jaw cancer; esophageal cancer; stomach cancer; colon cancer;
 KW lung cancer; liver cancer; gall-bladder cancer; pancreatic cancer;
 KW leukemia; liposarcoma; glioma.
 XX OS Homo sapiens.
 XX PN WO200237114-A1.
 XX PD 10-MAY-2002.
 XX PF 31-OCT-2001; 2001WO-JP009561.
 XX PR 01-NOV-2000; 2000JP-00335077.
 XX PA (GALP-) GALPHARMA CO LTD.
 PI Hirashima M, Yamauchi A, Kageshita T, Nakamura T, Nishi N;
 XX DR WPI; 2002-519265/55.
 PT Metastasis mechanism-based agents (anti-galectin 9 antibody) for
 PT detecting ability of cancer to metastasize in cells, uses galectin 9 as
 PT marker to detect cancer metastasis for diagnosis, cancer prevention and
 PT treatment.
 XX PS Example 1; Page 60-61; 68pp; Japanese.

XX The specification describes an agent for detecting the ability of cancers
 CC to metastasize. This agent comprises anti-galectin 9 antibody as the
 CC active ingredient. The agents and method are for detecting ability of
 CC cancer to metastasize in cancer cells, which are useful in the diagnosis,
 CC prevention and treatment of cancer. The cancer includes epithelial
 CC malignant tumours (tumourising or non-tumourising) in organs, tissues or
 CC blood. Such cancer can be 1 of the not less than 31 specifically claimed,
 CC e.g. skin cancer (including melanoma), breast cancer, ovarian cancer,
 CC uterus cancer, malignant tumour of the testis, prostate cancer, bladder
 CC cancer, kidney cancer, thyroid cancer, cancer of throat and larynx,
 CC tongue cancer, upper jaw cancer, esophageal cancer, stomach cancer, colon
 CC and rectum cancer, lung and bronchus cancer, liver cancer (including
 CC hepatocarcinoma and intrahepatic biliary cancer), extrahepatic biliary
 CC duct and gall-bladder cancer, pancreatic cancer, leukemia, malignant
 CC lymphoma, liposarcoma and glioma. The cancer cells are particularly
 CC breast cancer cells or melanoma cells. The present sequence represents a
 CC human protein, which is used in the course of the invention
 XX Sequence 355 AA;

SQ Query Match 52.4%; Score 163; DB 5; Length 355;
 Best Local Similarity 100.0%; Pred. No. 1.3e-155;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Query 149 TQTVIHTYQOSAPGMFSTPAIPPMYPHPAYPMFPTTLLGGLYPSKSILLSGTVPSSAQ 208
 Db 193 TQTVIHTYQOSAPGMFSTPAIPPMYPHPAYPMFPTTLLGGLYPSKSILLSGTVPSSAQ 252
 Query 209 RFHINLCSGNHIAFHINPREDENAVRNTQIDNSWGSERSLSPRKMPFTRGQSFVWILC 268
 Db 253 RFHINLCSGNHIAFHINPREDENAVRNTQIDNSWGSERSLSPRKMPFTRGQSFVWILC 312
 Query 269 EAHCILKVAVDGQHLPFYYHLRNLPTINLEVGDIQLTHVQT 311
 Db 313 EAHCILKVAVDGQHLPFYYHLRNLPTINLEVGDIQLTHVQT 355
 RESULT 11
 AC ADC53845
 ID ADC53845 standard; protein; 355 AA.
 XX AC ADC53845;
 XX DT 18-DEC-2003 (first entry)
 DE Human galectin 9 protein (long isoform).

XX galectin-9; nephritis; glomerular nephritis; antiinflammatory;
 XX glomerular infiltration; apoptosis; human.
 XX OS Homo sapiens.
 XX PN JP2002322082-A.
 XX PD 08-NOV-2002.
 XX PP 26-APR-2001; 2001JP-00129200.
 XX PR 26-APR-2001; 2001JP-00129200.
 XX PA (PROT-) PROTEGENE KK.
 XX DR 2003-367092/35.
 XX PT Agents for prevention and treatment of nephritis, comprise galectin-1, galectin-3, or galectin-9, by inhibition of intraglomerular infiltration of leukocytes, CD8 positive cells, and induction of apoptosis of CD8 positive cells.
 XX PS Disclosure; SEQ ID NO 4; 31pp; Japanese.
 XX This invention relates to the use of novel mammal derived galectin-1, (G1), -3 (G3) and -9 (G9) proteins as effective ingredients for prevention and treatment of nephritis. The invention discloses agents for prevention and treatment of nephritis, particularly glomerular nephritis and may have antiinflammatory activities. The method of the invention inhibits glomerular infiltration of leukocytes, CD8 positive cells and apoptosis of CD8 positive cells. The method and sequences of the invention may be used for prevention and treatment of nephritis, particularly glomerular nephritis including inhibition of glomerular infiltration of leukocytes, CD8 positive cells and apoptosis of CD8 positive cells. The present sequence represents the human galectin 9 protein (long isoform) used in the exemplification of the present invention.
 XX Sequence 355 AA;
 Query Match 52.4%; Score 163; DB 7; Length 355;
 Best Local Similarity 100.0%; Pred. No. 1.3e-155;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 149 TQTVIHTVQSARGQMSTPAI PPMYPPHAYPMPFTITLGLYPSKSILLSGTVLPSAQ 208
 Db 193 TQTVIHTVQSARGQMSTPAI PPMYPPHAYPMPFTITLGLYPSKSILLSGTVLPSAQ 252
 Qy 209 RFHINLCSGNHTAFHLNPRDENAVYNTQIDNSNGSEERSLPRKMPFVRGQSFSYWILC 268
 Db 253 RFHINLCSGNHTAFHLNPRDENAVYNTQIDNSNGSEERSLPRKMPFVRGQSFSYWILC 312
 Qy 269 EAHCLKVAVDGQHLFEYVHRLNPLPTINRLEVGGDQLTHVQT 311
 Db 313 EAHCLKVAVDGQHLFEYVHRLNPLPTINRLEVGGDQLTHVQT 355
 RESULT 12
 ADE62929 DT 29-JAN-2004 (first entry)
 ID ADE62929 standard; protein; 355 AA.
 XX AC ADE62929;
 XX DT 29-JAN-2004 (first entry)
 XX DB Human Protein 000182, SEQ ID NO 8863.
 XX OS Homo sapiens.
 XX KW pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 XX PN WO2003016475-A2.
 XX PD 27-FEB-2003.
 XX PP 14-AUG-2002; 2002WO-US025765.
 XX PR 14-AUG-2001; 2001US-0312147P.
 XX PR 01-NOV-2001; 2001US-0346582P.
 XX PR 26-NOV-2001; 2001US-0333347P.
 XX PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX PI Woolf C, D'urso D, Beffort K, Costigan M;
 XX DR 2003-268312/26.
 XX DR GENBANK; 000182.
 XX PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
 XX PS Claim 1; Page: 1017pp; English.
 XX CC The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 355 AA;
 Query Match 52.4%; Score 163; DB 7; Length 355;
 Best Local Similarity 100.0%; Pred. No. 1.3e-155;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 149 TQTVIHTVQSARGQMSTPAI PPMYPPHAYPMPFTITLGLYPSKSILLSGTVLPSAQ 208
 Db 193 TQTVIHTVQSARGQMSTPAI PPMYPPHAYPMPFTITLGLYPSKSILLSGTVLPSAQ 252
 Qy 209 RFHINLCSGNHTAFHLNPRDENAVYNTQIDNSNGSEERSLPRKMPFVRGQSF SYWILC 268
 Db 253 RFHINLCSGNHTAFHLNPRDENAVYNTQIDNSNGSEERSLPRKMPFVRGQSF SYWILC 312
 Qy 269 EAHCLKVAVDGQHLFEYVHRLNPLPTINRLEVGGDQLTHVQT 311
 Db 313 EAHCLKVAVDGQHLFEYVHRLNPLPTINRLEVGGDQLTHVQT 355
 RESULT 13
 ADE62929 DT 29-JAN-2004 (first entry)
 ID ADE62929 standard; protein; 355 AA.
 XX AC ADE62929;
 XX DT 29-JAN-2004 (first entry)
 XX DB Human Protein 000182, SEQ ID NO 8863.
 XX OS Homo sapiens.
 XX KW pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 RESULT 13
 ADD48101

| | | | | |
|----|---|----------------------------|-----|--|
| ID | ADD48101 | standard; protein; 355 AA. | Qy | 149 TQTVIHTYQSAPGOMFSTPAIPPMMPHPPAYPMPFITITLGGLYPSKSILLSCTVLPSEQ 208 |
| XX | | | Db | 193 TQTVIHTYQSAPGOMFSTPAIPPMMPHPPAYPMPFITITLGGLYPSKSILLSCTVLPSEQ 252 |
| AC | | | Qy | 209 RFHINLCSANHIAFHLPNPRFDENAVRNTQIDNSWGSERSLPRKMPFVRGQSFSSVWILC 268 |
| XX | 02-DEC-2004 (revised) | | Db | 253 RFHINLCSANHIAFHLPNPRFDENAVRNTQIDNSWGSERSLPRKMPFVRGQSFSSVWILC 312 |
| DT | 29-JAN-2004 (first entry) | | Qy | 269 EAHCILKVAVDGQHLFYTHRLRNLPNTINLEVGQDIDQLTHVQT 311 |
| XX | Human Protein O00182, SEQ ID NO 13799. | | Db | 313 EAHCILKVAVDGQHLFYTHRLRNLPNTINLEVGQDIDQLTHVQT 355 |
| XX | Human; pain; neuronal tissue; gene therapy; | | | |
| XX | spinal segmental nerve injury; chronic constriction injury; CCI; | | | |
| XX | spared nerve injury; SNI; Chung. | | | |
| OS | Homo sapiens. | | | |
| OS | Unidentified. | | | |
| XX | WO2003016475-A2. | | ID | ADG91608 standard; protein; 355 AA. |
| XX | 27-FEB-2003. | | AC | ADG91608; |
| XX | 14-AUG-2002; 2002WO-US025765. | | XX | 11-MAR-2004 (first entry) |
| XX | 14-AUG-2001; 2001US-0312147P. | | XX | Human lectin galactoside binding protein (LGAL) #2. |
| PR | 01-NOV-2001; 2001US-0346382P. | | XX | KW Human; lectin galactoside binding protein; LGAL; CHK pathway; cancer; gene therapy. |
| PR | 26-NOV-2001; 2001US-0333347P. | | XX | KW |
| PA | (GBHO) GEN HOSPITAL CORP. | | OS | Homo sapiens. |
| PA | (FARB) BAYER AG. | | XX | |
| XX | Woolf C, D'urso D, Befort K, Costigan M; | | Key | |
| XX | WPI; 2003-26812/26. | | XX | 16. .147 Galactose binding lectin domain |
| DR | GENBANK; Q00182. | | FT | /note = Galactose binding lectin domain |
| PT | New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal. | | FT | 226. .335 Galactose binding lectin domain |
| PS | Example 1, Page: 1017pp; English. | | FT | /note = Galactose binding lectin domain |
| XX | The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (described in Table 3 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp://wipo.int/pub/published_pct_sequences . | | XX | Location/Qualifiers |
| XX | Sequence 355 AA; | | XX | |
| SQ | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | XX | |
| | Query Match 52.4%; Score 163; DB 7; Length 355; | | XX | |
| | Best Local Similarity 100.0%; Pred. No. 1.3e-155; | | XX | |
| | Matches 16 | | | |

Db 193 TQTVIHTVQAPGQMFSTPAIPPMYPHAPYMPMPPITLGLYPSKSTILSGTVLPSAQ 252
 Qy 209 RFHINICSGNIIAFLHNPREFDENAVRNTQIDNSWGSBEERSLPRKMPFRGQSFVWILC 268
 Db 253 RFHINICSGNIIAFLHNPREFDENAVRNTQIDNSWGSBEERSLPRKMPFRGQSFVWILC 312
 Qy 269 EAHCKVAVDGQHLPFYYHRLRNLPPTINRLEVGGDQLQLTHVQT 311
 Db 313 EAHCKVAVDGQHLPFYYHRLRNLPPTINRLEVGGDQLQLTHVQT 355

RESULT 15

AAE13847 standard; protein; 378 AA.

XX AAE13847;

XX 26-FEB-2002 (first entry)

XX Human lung tumour-specific protein 21871.

DE Human lung tumour protein; immunostimulant; cytostatic; gene therapy; antisense-therapy; vaccine; immune response; lung cancer; 21871.

OS Homo sapiens.

XX FH Key

FT Misc-difference 182 .183

FT /note= "Encoded by RTCC"

XX PN WO200172295-A2.

XX PD 04-OCT-2001.

XX PP 28-MAR-2001; 2001WO-US009991.

XX PR 29-MAR-2000; 2000US-00538037.

PR 05-JUN-2000; 2000US-00588937.

PR 18-AUG-2000; 2000US-00640878.

PR 22-SEP-2000; 2000US-0234517P.

PR 01-NOV-2000; 2000US-00704512.

PR 14-DEC-2000; 2000US-00738973.

XX PA (CORTI-) CORIXA CORP.
 XX PI Reed SG, Lodes MJ, Mohamath R, Secrist H, Benson DR, Indrias CY;
 PI Henderson RA, Flings SP, Algate PA, Elliot M, Mannion J, Kalos MD;
 DR WPI: 2001-639201/73.
 DR N-PSDB; AAD23459.XX PT New human lung-specific polynucleotides and polypeptides for the
 PT diagnosis and treatment of disease e.g. lung cancer.
 PS Disclosure; Page 331; 378pp; English.
 XX CC The invention relates to isolated lung tumour-specific proteins and their
 CC corresponding cDNA molecules. Lung tumour-specific proteins and their
 CC antigen-presenting cells are useful for stimulating and/or expanding T
 CC cells specific for a tumour protein, and for inhibiting the development
 CC of cancer. The invention also relates to a composition useful for
 CC stimulating an immune response, and for treating cancer. The lung tumour
 CC specific oligonucleotide is useful in gene therapy and for diagnosis,
 CC detection and treatment of lung cancer. The present sequence is human
 CC lung tumour-specific protein
 XX SQ Sequence 378 AA;

Query Match 52.4%; Score 163; DB 4; Length 378;

Best Local Similarity 100.0%; Pred. No. 1.4e-155;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SQSearch completed: July 13, 2005, 07:50:31
 Job time : 167 secs

Db 149 TQTVIHTVQAPGQMFSTPAIPPMYPHAPYMPMPPITLGLYPSKSTILSGTVLPSAQ 208
 Db 216 TQTVIHTVQAPGQMFSTPAIPPMYPHAPYMPMPPITLGLYPSKSTILSGTVLPSAQ 275
 Qy 209 RFHINICSGNIIAFLHNPREFDENAVRNTQIDNSWGSBEERSLPRKMPFRGQSFVWILC 268
 Db 276 RFHINICSGNIIAFLHNPREFDENAVRNTQIDNSWGSBEERSLPRKMPFRGQSFVWILC 335
 Qy 269 EAHCKVAVDGQHLPFYYHRLRNLPPTINRLEVGGDQLQLTHVQT 311
 Db 336 EAHCKVAVDGQHLPFYYHRLRNLPPTINRLEVGGDQLQLTHVQT 378

115 page blank (uspro)

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protein - protein search, using SW model

on: July 13, 2005, 07:46:47 ; Search time 40 Seconds
(without alignments)
748.085 Million cell updates/sec

title: US-09-263-689-4

perfect score: 311

sequence: 1 MAFSGSQAPYLSPAVPFSGT. LPTINRLEVGGDIQLTHVQT 311

oring table: OLIGO

A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-245 <MEH>
 A;Cross-references: GB:X78879; NID:9535082; PIDN:CAA55479.1; PID:9535083
 C;Superfamily: beta-galactoside-binding lectin
 C;Keywords: lectin

Query Match 3.9%; Score 12; DB 2; Length 245;
 Best Local Similarity 100.0%; Pred. No. 0.00012; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; DB 2; Length 324;
 Qy 55 GNDIAFHNPFRF 66
 Db 147 GNDIAFHNPFRF 158

RESULT 3

A54889
 IgE-binding Protein - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A54889; A3148
 R;Albrant, M.; Orida, N.K.; Liu, F.T.; Liu, F.T.; Albrant, K.; Mende, E.; Orida, N.K.
 Proc. Natl. Acad. Sci. U.S.A. 84, 6859-6863, 1987
 A;Title: An IgE-binding protein with a distinctive repetitive sequence and homology with
 A;Accession number: A54889; MUID:88016189; PMID:2958848
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-262 <ALB>
 A;Cross-references: UNIPROT: P08699; GB:J02962; NID:9203173; PIDN:AAA40828.1; PID:9203174
 Proc. Natl. Acad. Sci. U.S.A. 82, 4100-4104, 1985
 A;Title: Identification of an IgE-binding Protein by molecular cloning.
 A;Accession number: A23148; MUID:85216641; PMID:3858867
 A;Accession: A23148
 A;Molecule type: mRNA
 A;Residues: 1-262 <LU>
 A;Cross-references: GB: M13697; NID:9204727; PIDN:AAA41378.1; PID:9204728
 C;Superfamily: beta-galactoside-binding lectin
 C;Keywords: lectin; phosphoprotein

Query Match 3.9%; Score 12; DB 2; Length 262;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; DB 2; Length 324;
 Qy 55 GNDIAFHNPFRF 66
 Db 164 GNDIAFHNPFRF 175

RESULT 4

A46631
 lactose-binding lectin L-36 - rat
 N;Alternate names: galactin-4
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A46631; S8096
 R;Ioda, Y.; Harriman, J.; Gitt, M.A.; Turck, C.W.; Burlingsame, A.L.; Barondes, S.H.; Leff
 J. Biol. Chem. 268, 5939-5939, 1993
 A;Title: Soluble lactose-binding lectin from rat intestine with two different carbohydrate
 A;Accession number: A46631; MUID:93194902; PMID:8449956
 A;Status: preliminary
 A;Molecule type: nucleic acid
 A;Residues: 1-324 <ODA>
 A;Cross-references: UNIPROT: P38552; GB: M73553; NID: 9294571; PIDN: AAA41505.1; PID: 9294572
 A;Experimental source: intestine backbone (NCBIN: 128410)
 A;Note: sequence extracted from NCBI backbone (NCBIN: 128409, NCBI: 128410)
 R;Tardy, F.; Deviller, P.; Louiset, P.; Martin, A.
 FEBS Lett. 359, 169-172, 1995
 A;Title: Purification and characterization of the N-terminal domain of galactin-4 from
 A;Reference number: S63096; MUID: 9517227; PMID: 7867792

RESULT 5

S08576
 lectin - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S08576
 R;Raz, A.; Carmi, P.; Pazerini, G.
 Cancer Res. 48, 645-649, 1988
 A;Title: Expression of two different endogenous galactoside-binding lectins sharing sequ
 A;Reference number: S07162; MUID: 8808093; PMID: 3335026
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-139 <RAZ>
 A;Cross-references: UNIPROT: Q61357
 C;Superfamily: beta-galactoside-binding lectin

Query Match 2.6%; Score 8; DB 2;
 Best Local Similarity 100.0%; Pred. No. 1.8%;
 Matches 8; Conservative 0; Mismatches 0; DB 2; Length 139;
 Qy 59 AFHFNPFRF 66
 Db 72 AFHFNPFRF 79

RESULT 6

JC4300
 galectin-3 - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
 C;Accession: JC4300
 R;Gaudin, J.-C.; Monsigny, M.; Legrand, A.
 Gene 163, 249-252, 1995
 A;Title: Cloning of the cDNA encoding rabbit galectin-3.
 A;Reference number: JC4300; MUID: 96011642; PMID: 7590275
 A;Accession: JC4300
 A;Molecule type: mRNA
 A;Residues: 1-242 <GAU>
 A;Cross-references: UNIPROT: P47845; GB: U06470; NID: 9606794; PIDN: AAC48491.1; PID: 9606795
 A;Experimental source: vascular smooth muscle cells
 A;Note: The authors translated the codon TRC for residue 155 as Leu
 C;Comment: This protein has the functions on cell adhesion and proliferation. It is a su
 A;Gene: Igale3
 C;Superfamily: beta-galactoside-binding lectin
 C;Keywords: muscle

Query Match 2.6%; Score 8; DB 2;
 Best Local Similarity 100.0%; Pred. No. 2.9%;
 Matches 8; Conservative 0; Mismatches 0; DB 2; Length 242;
 Qy 59 AFHFNPFRF 66
 Db 148 AFHFNPFRF 155

RESULT 7

A35620
galactin 3 - human
N;Alternate names: CBP '35; epithelial-specific lectin 35; galactoside-binding lectin L-2
C;Species: Homo sapiens (man)
C;Date: 12-Oct-1990 #sequence revision 12-Oct-1990 #text_change 09-Jul-2004
C;Accession: A35820; JQ0916; A47473; A36071; A49800
R;Robertson, M.W.; Albrandt, K.; Keller, D.; Liu, F.T.
Biochemistry 29, 8093-8100, 1990
A;Title: Human IgE-binding protein: a soluble lectin exhibiting a highly conserved inter
A;Accession: A35820; MUID:91084480; PMID:2261464
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-250 <ROB>
A;Cross-references: UNIPROT:P17931; GB:M57710; PIDN:AAA35607.1; PID:g179531
R;Oda, Y.; Loeffler, H.; Sakakura, Y.; Kasai, K.; Barondes, S.H.
Gene 99, 279-283, 1991
A;Title: Human breast carcinoma cDNA encoding a galactoside-binding lectin homologous to
A;Accession: JQ0916; MUID:91216471; PMID:2022338
A;Accession: JQ0916
A;Molecule type: mRNA
A;Residues: 1-250 <ROB>
A;Cross-references: GB:M36682; PID:9186921; PID:AAA16163.1; PID:g186922
R;Lotz, M.M.; Andrews, J.T.; C.W.; Korzelius, C.A.; Lee, E.C.; Steele Jr., G.D.; Clarke, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 3466-3470, 1993
A;Title: Decreased expression of Mac-2 (carbohydrate binding protein 35) and loss of its
A;Reference number: A47473; MUID:9323418; PMID:7682704
A;Accession: A47473
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-63, 'P', 65-97, 'T', 99-250 <LOT>
A;Cross-references: GB:S59012; NID:g298601; PIDN:AAAB26229.1; PID:g299602
A;Experimental source: normal colonic mucosa; colon carcinoma, cell line clone A
A;Note: sequence extracted from NCBI backbone (NCBIN:129689, NCBIPI:129692)
R;Cheravil, B.J.; Chaitovitz, S.; Wong, C.; Pillai, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 7324-7328, 1990
A;Title: Molecular cloning and chromosomal mapping of a human galactoside-binding protein
A;Reference number: A356071; MUID:90384999; PMID:2402311
A;Accession: A36071
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-32, 'Q', 34, 'L', 37, 'RGFLSNGL', 46, 'RAGT', 51, 'R', 53-63, 'P', 65-87, 89-250 <CHE>
A;Cross-references: GB:35365; NID:91196441
A;Note: the sequence is revised in GenBank entry HUMMAC2, release 113.0. PIDN:AAA88086.1
R;Raz, A.; Carmi, P.; Raz, T.; Hogan, V.; Mohamed, A.; Wolman, S.R.
Cancer Res. 51, 2173-2178, 1991
A;Title: Molecular cloning and chromosomal mapping of a human galactoside-binding protein
A;Reference number: A49800; MUID:91183475; PMID:2009335
A;Accession: A49800
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-32, 'Q', 34, 'LPGASYPGRAYPGLSNMAPPATMHRVELTRSTCWLSLRTQ', 86-104, 'A', 106, N
A;Cross-references: GB:M64303; NID:9413862
A;Map position: 1P13-1P13
C;Superfamily: betagalactoside-binding lectin
C;Keywords: lectin; nucleus; phosphoprotein
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 9
A45983
lactose-binding lectin Mac-2 - mouse
C;Species: Mus musculus (house mouse)
C;Accession: A45983
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
R;Rosenberg, I.M.; Iyer, R.; Chiodino, C.; Pillai, S.
J. Biol. Chem. 268, 12393-12400, 1993
A;Title: Structure of the murine Mac-2 gene. Splice variants encode proteins lacking fur
A;Reference number: A45983; MUID:93286070; PMID:8509379
A;Accession: A45983
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-264 <ROS>
A;Cross-references: UNIPROT:Q8C253; GB:L08649
C;Genetics:
A;Introns: 6/3; 128/3; 158/2; 209/2; 213/3
C;Superfamily: betagalactoside-binding lectin
Query Match 2.6%; Score 8; DB 2; Length 264;
Best Local Similarity 100.0%; Pred. No. 3.2; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 8
A2651
galactose-specific lectin - mouse

RESULT 15

C97362 protein sensor protein (AF042096) [Imported] - Agrobacterium tumefaciens (strain C58, Ce
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: C97362
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; PMID:21608551; PMID:11743194
A;Accession: C97362
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-881 <KUR>
A;Cross references: UNIPROT:Q8UJAI; PIDN:AAK85852.1; PID:gi1514889; GSFPDB:G
C;Genetics:
A;Gene: AGR_C_44
A;Map position: circular chromosome

Query Match 2.6%; Score 8; DB 2; Length 881;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 ILLSGTTL 204
Db 69 ILLSGTTL 76

Search completed: July 13, 2005, 08:02:31
Job time : 42 secs

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